GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 00:16:08 ; Search time 4401.47 Seconds
(without alignments)
10982.631 Million cell updates/sec

Title: US-09-001-737-7
Perfect score: 1661
Sequence: 1 GAATTCGGCTTCATATGGCA.....TGGGCGGATAAGCCGAATTC 1661

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	1622.2	97.7	10389	1	AE006627	AE006627 Streptoco
c 2	1607.8	96.8	53291	1	AE014170	AE014170 Streptoco
c 3	1604.6	96.6	11576	1	AE010115	AE010115 Streptoco
4	1413.4	85.1	2683	1	SPGROELGN	X89236 S.pyogenes
5	1413.4	85.1	2683	6	AX148805	AX148805 Sequence
6	1170.4	70.5	1421	1	AY121365	AY121365 Streptoco
7	1140.4	68.7	1306	6	AX148806	AX148806 Sequence
8	1128.8	68.0	1421	1	AY121364	AY121364 Streptoco
9	1125	67.7	1422	1	AY121366	AY121366 Streptoco
10	1122.6	67.6	1305	6	AX148809	AX148809 Sequence
11	1118	67.3	1415	1	AY121367	AY121367 Streptoco
12	1104.2	66.5	2054	1	AF389514	AF389514 Streptoco
13	1080	65.0	1384	1	AY121363	AY121363 Streptoco
14	1076.4	64.8	2324	1	AF389516	AF389516 Streptoco
15	1068.6	64.3	2320	1	AF389515	AF389515 Streptoco
16	1064.6	64.1	2020	1	AF389517	AF389517 Streptoco
17	1053.8	63.4	1718	1	AF325222	AF325222 Streptoco
18	1050.8	63.3	2639	1	AF378195	AF378195 Streptoco
19	1050.8	63.3	2750	1	AF378196	AF378196 Streptoco
20	1039.2	62.6	1623	6	AX194119	AX194119 Sequence
c 21	1038.6	62.5	21494	2	SPNEU1924	AL449946 Streptoco
22	1038.4	62.5	1926	6	AX073958	AX073958 Sequence
23	1037	62.4	2107	1	AF325449	AF325449 Streptoco
24	1037	62.4	2107	6	AX148804	AX148804 Sequence
25	1036	62.4	1647	6	AX194338	AX194338 Sequence
26	1035.4	62.3	5365	6	BD003757	BD003757 Polynucle
c 27	1035.4	62.3	11318	1	AE008538	AE008538 Streptoco
c 28	1035.4	62.3	13103	1	AE007482	AE007482 Streptoco
29	1030.6	62.0	2401	1	AF117741	AF117741 Streptoco
30	1030.6	62.0	2401	6	AX148803	AX148803 Sequence
31	1014	61.0	3666	1	AF338228	AF338228 Streptoco
32	1013.2	61.0	1963	1	AY038047	AY038047 Streptoco
33	1013.2	61.0	2490	1	AF378197	AF378197 Streptoco
34	955	57.5	12560	1	AE006276	AE006276 Lactococc
35	948.6	57.1	2267	1	LLGROESEL	X71132 L.lactis gr
36	942.2	56.7	2187	1	AY029215	AY029215 Lactococc
37	942	56.7	3120	1	AF335185	AF335185 Enterococ
38	844.6	50.8	2853	1	AB073399	AB073399 Tetrageno
39	840.4	50.6	2834	1	AB028452	AB028452 Bacillus
40	838.8	50.5	2309	1	BACSGROESL	L10132 Bacillus st
41	832	50.1	1901	6	AX416527	AX416527 Sequence
42	824	49.6	213251	6	AX413015	AX413015 Sequence
c 43	824	49.6	349980	6	AX417047	AX417047 Sequence
44	822.4	49.5	2156	1	AF335323	AF335323 Listeria
c 45	822.4	49.5	295050	1	AL591982	AL591982 Listeria

ALIGNMENTS

RESULT 1
AE006627/c
LOCUS AE006627 10389 bp DNA linear BCT 01-JUN-2001
DEFINITION Streptococcus pyogenes M1 GAS strain SF370, section 156 of 167 of the complete genome.
ACCESSION AE006627 AE004092
VERSION AE006627.1 GI:13623059
KEYWORDS .
SOURCE Streptococcus pyogenes M1 GAS.
ORGANISM Streptococcus pyogenes M1 GAS
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
REFERENCE 1 (bases 1 to 10389)
AUTHORS Ferretti,J.J., McShan,W.M., Adjic,D., Savic,D., Savic,G., Lyon,K., Primeaux,C., Sezate,S.S., Surorov,A.N., Kenton,S., Lai,H., Lin,S.,

Qian,Y., Jia,H.G., Najar,F.Z., Ren,Q., Zhu,H., Song,L., White,J., Yuan,X., Clifton,S.W., Roe,B.A. and McLaughlin,R.E.
TITLE Complete genome sequence of an M1 strain of Streptococcus pyogenes
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (8), 4658-4663 (2001)
MEDLINE 21192684
PUBMED 11296296
REFERENCE 2 (bases 1 to 10389)
AUTHORS Ferretti,J.J., McShan,W.M., Adjic,D., Savic,D., Savic,G., Lyon,K., Primeaux,C., Sezate,S.S., Surorov,A.N., Kenton,S., Lai,H., Lin,S., Qian,Y., Jia,H.G., Najar,F.Z., Ren,Q., Zhu,H., Song,L., White,J., Yuan,X., Clifton,S.W., Roe,B.A. and McLaughlin,R.E.
TITLE Direct Submission
JOURNAL Submitted (10-APR-2001) Department of Microbiology and Immunology, University of Oklahoma Health Sciences Center, 940 SL Young Blvd, Oklahoma City, OK 73104, USA

FEATURES Location/Qualifiers

source 1. .10389
/organism="Streptococcus pyogenes M1 GAS"
/strain="SF370"
/serotype="M1"
/db_xref="taxon:160490"

gene complement(75. .1799)
/gene="SPy2065"

CDS complement(75. .1799)
/gene="SPy2065"
/note="Best Blastp hit = prf||2109195A chondroitin ABC lyase [Proteus vulgaris]"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="AAK34725.1"
/db_xref="GI:13623060"
/translation="MNYLGFFENPLAIYDIIVKKNIESWGLLMTKPFHHKKLKQITII
AATSLFLFLIGGAFYYSKNHCINAYLKARSAQSGPVFENIKAYLVWDDTNEQITNDEA
MYTKFRRYSQKELRQKKQDLKAASQDSAVQVKSVGRRFWIFPDYRIAIKPMDLTIKTN
VPQADVLLNQKKVAVSDSEQFSVKLDRLPTAEYTASIRGKHNGRNIKVNKSYDGDNPV
LDLSVSFRTFLVTSNAKQGDLYFDDNHIGTLKDGQLQVEDYPVTENAQAYMKTTFPDG
ELRSQKYALADVEEGATLEILVTDLLEEDKAGELLVSAFDQLMHYLSTGQDSSNLRSV
FEAGSSNAFYRGLKESIKAKFQTDTRKASRLNIPSILLTTMTQVGKTTYVLDFTATYE
FLYDKSTDPEQHTSGHINQDLTGKVTVKKVGQHYLISQSGSKNITVVKEDNQLKAPSV
FPESILGTWTGQANGLSIHMSLASDGTITTKVEDQKGNRSKETRTAKISKVEDKGNGF
YLYTPDPGSDISALVPEGGLGGANVKYAYGFKISGKTASPVVWQAALTHEFDYTKPLS
GVTLQKQP"

gene 1962. .3458
/gene="SPy2066"

CDS 1962. .3458
/gene="SPy2066"
/note="Best Blastp hit = emb|CAA66893.1| (X98238) putative; orf1 [Lactobacillus sakei]"
/codon_start=1
/transl_table=11
/product="putative dipeptidase"
/protein_id="AAK34726.1"
/db_xref="GI:13623061"
/translation="MINKKISLGVLSILTAFSLQSVSYACTGFIIGKDLTKDGSLLYG
RTEDLEPHHNKNFIVRLAKDNPAGEKWKDLSNGFEYPLPEHSYRYSAIPDVTPNKGVY
DEAGFNEFGVSMSATVSASANDAIQKIDPYVKNGLAESSMTSVILPSVKTAREGVALI
AKIVTEKGAAEGNIVTLADKDGIWYMEILSGHQYVAIKFPDDKYAVFPNTFYLGHVDF
NDKENTIASEDVEKVAKKAKSYTEVDGKFHIAKSYNPPLNDANRSRSFSGIKSLDPDS
KVTYKDSNYELLQSTDKTFSLEDAMKLQRNRFEGLDLKPLDQMALDGKGKPKSKKAVK
GYAYPISNPNVMEAHIFQLKKDIPAELGGVMWLSIGSPRNAPYLPYLGNISRTYEAYQ
EKSTQYNDKSWYWTVSHINDLVAAHPKPFGTKVIDEMKGLEKTWIAEQDKSTKEISDL
VVSDPKAAQEKADKISLDRAEKTFKRLKAIEAKLVKEKPKNKKGLNRS"

gene complement(4661. .6292)
/gene="groEL"
/note="SPy2070"

CDS complement(4661. .6292)
/gene="groEL"
/note="The N-terminal amino acid sequence of this ORF has been determined from a spot isolated by 2-D gel electrophoresis from another strain of S. pyogenes. Hogan, D. A., Whitton, M. M., Rogers, J. and R. A. VanBogelen. 2000. Two-dimensional gel electrophoresis map of Streptococcus pyogenes proteins. Unpublished data.; Best Blastp hit = emb|CAA61520.1| (X89236) heat shock protein [Streptococcus pyogenes]"
/codon_start=1
/transl_table=11
/product="heat shock protein (chaperonin)"
/protein_id="AAK34727.1"
/db_xref="GI:13623062"
/translation="MAKDIKFSADARAAMVRGVDMLADTVKVTLGPKGRNVVLEKAFG
SPLITNDGVTIAKEIELEDHFENMGAKLVSEVASKTNDIAGDGTTTATVLTQAIVHEG
LKNVTAGANPIGIRRGIETATATAVEALKAIAQPVSGKEAIAQVAAVSSRSEKVGEYI
SEAMERVGNDGVITIEESRGMETELEVVEGMQFDRGYLSQYMVTDNEKMVADLENPFI
LITDKKVSNIQDILPLLEEVLKTNRPLLIIADDVDGEALPTLVLNKIRGTFNVVAVKA
PGFGDRRKAMLEDIAILTGGTVITEDLGLELKDATMTALGQAAKITVDKDSTVIVEGS
GSSEAIANRIALIKSQLETTTSDFDREKLQERLAKLAGGVAVIKVGAPTETALKEMKL
RIEDALNATRAAVEEGIVAGGGTALITVIEKVAALELEGDDATGRNIVLRALEEPVRQ
IALNAGYEGSVVIDKLKNSPAGTGFNAATGEWVDMIKTGIIDPVKVTRSALQNAASVA
SLILTTEAVVANKPEPATPAPAMPAGMDPGMMGGP"

gene complement(6328. .6618)
/gene="groES"
/note="SPy2072"

CDS complement(6328. .6618)
/gene="groES"
/note="The N-terminal amino acid sequence of this ORF has been determined from a spot isolated by 2-D gel electrophoresis from another strain of S. pyogenes. Hogan, D. A., Whitton, M. M., Rogers, J. and R. A. VanBogelen. 2000. Two-dimensional gel electrophoresis map of Streptococcus pyogenes proteins. Unpublished data.; Best Blastp hit = gb|AAF75592.1|AF214488_2 (AF214488) GroES [Lactobacillus johnsonii]"
/codon_start=1
/transl_table=11
/product="heat shock protein - cochaperonin"
/protein_id="AAK34728.1"
/db_xref="GI:13623063"
/translation="MLKPLGDRVVVRFDDEKEQTVGGFVLAGTHKESTRKATVLAVSE
TGVRTITGDSVLPSVSVGQEVLVENGHDLEVTVDDEKVSIIRESDIIAIVTK"

gene complement(6796. .9240)
/gene="clpC"
/note="SPy2073"

CDS complement(6796. .9240)
/gene="clpC"
/note="Best Blastp hit = gb|AAC44446.1| (U40604) ClpC ATPase [Listeria monocytogenes]"
/codon_start=1
/transl_table=11
/product="putative endopeptidase Clp ATP-binding chain C"
/protein_id="AAK34729.1"
/db_xref="GI:13623064"
/translation="MIMYSTKMQDIFRQAQFQAARFDSHCLETWHVLLAMVAVDNSLA
NMILSEYDAQVAIEEYEAAAILAMGKTPKEQLSRVDFRPQSKTLTNLLAFAQAISQIT
RDQEVGSEHVLFAILLNPDIMASRLLEIAGYQIKDNGNGQPRLADLRKAIERHAGYSK
EMIKAIHELRKPKKTKTQGTFSDMMKPPSTAGELSDFTRDLTEMARQGLLESVIGRDQ
EVSRMIQVLSRKTKNNPVLVGDAGVGKTALAYGLAQRIANGAIPYELKEMRVLELDMM
SVVAGTRFRGDFEERMNQIIDDIEADGQIILFVDELHTIMGSGSGIDSTLDAANILKP
ALSRGTLHMVGATTQEEYQKHIEKDAALSRRFAKILIEEPNTEDAYQILMGLKLSYET
YHNVSISNEAVKTAVKMAHRYLTSKNLPDSAIDLLDEASAAVQNMVKKSAPETLTPID
QALINGDMKKVSRLLAKEAKGQMRKPTPVTEDDILATLSKLSGIPLEKLTQADSKKYL
NLEKELHKRVIGQDAAVTAISRAIRRNQSGIRTGKRPIGSFMFLGPTGVGKTELAKAL
AEVLFDDEAALIRFDMSEYMEKFAASRLNGAPPGYVGYDEGGELTQKVRNKPYSVLLF
DEVEKAHPDIFNVLLQVLDDGILTDSRGRKVDFSNTIIIMTSNLGATALRDDKTVGFG
VKDIHQDHQAMEKRILEELRKTYRPEFINRIDEKVVFHSLTQDNMRDVVKIMVQPLIT
TLAEKGITLKIQPLALKHLSEVGYDEHMGARPLRRTLQTEIEDKLSELILSRELTSGH
TLKIGLSHGKLTFHIA"

gene complement(9240. .9701)
/gene="ctsR"
/note="SPy2074"

CDS complement(9240. .9701)
/gene="ctsR"
/note="Best Blastp hit = sp|P37568|CTSR_BACSU TRANSCRIPTIONAL REGULATOR CTSR >gi|2127052|pir||S66112 transcription repressor ctsR - Bacillus subtilis

```
                     >gi|467471|dbj|BAA05317.1| (D26185) unknown [Bacillus
                     subtilis] >gi|2632350|emb|CAB11859.1| (Z99104)
                     transcriptional regulator [Bacillus subtilis]"
                     /codon_start=1
                     /transl_table=11
                     /product="putative transcriptional regulator"
                     /protein_id="AAK34730.1"
                     /db_xref="GI:13623065"
                     /translation="MPTKNTSDSIEEYIKELLAKSGIAEIKRSMLADSFQVVPSQINY
                     VIKTRFTESRGYEVESKRGGGGYIRIAKVHFSDKHHLIGNLMATIEDCISEQVFTDSI
                     QLLFDEHLLTEREGNIILAVASDDVLGTDGSTIRARMLYRLLQRIDRKGSN"
     gene            complement(9897. .10100)
                     /gene="csp"
                     /note="SPy2077"
     CDS             complement(9897. .10100)
                     /gene="csp"
                     /note="Best Blastp hit = emb|CAA76697.1| (Y17216) cold
                     shock protein D [Lactococcus lactis]"
                     /codon_start=1
                     /transl_table=11
                     /product="putative cold shock protein"
                     /protein_id="AAK34731.1"
                     /db_xref="GI:13623066"
                     /translation="MAQGTVKWFNAEKGFGFISTENGQDVFAHFSAIQTNGFKTLEEG
                     QKVAFDVEEGQRGPQAVNITKLA"
BASE COUNT     3077 a    2210 c    1855 g    3247 t
ORIGIN

  Query Match             97.7%;  Score 1622.2;  DB 1;  Length 10389;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1624;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      13 ATATGGCAAAAGAAATCAAATTTTCAGCAGATGCGCGTGCTGCCATGGTGCGCGGAGTTG 72
           |||||||||||||| || ||||||||||||||||||||||||||||||||||||||||||
Db    6294 ATATGGCAAAAGATATTAAATTTTCAGCAGATGCGCGTGCTGCCATGGTGCGCGGAGTTG 6235

Qy      73 ATATGTTAGCAGATACCGTCAAAGTAACGCTTGGTCCTAAAGGGCGCAATGTTGTTCTTG 132
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    6234 ATATGTTAGCAGATACCGTCAAAGTAACGCTTGGTCCTAAAGGGCGCAATGTTGTTCTTG 6175

Qy     133 AAAAAGCTTTTGGTTCTCCCTTAATTACTAATGACGGGGTAACCATTGCTAAAGAGATCG 192
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    6174 AAAAAGCTTTTGGTTCTCCCTTAATTACTAATGACGGGGTAACCATTGCTAAAGAGATCG 6115

Qy     193 AATTAGAAGATCATTTTGAAAACATGGGAGCAAAATTGGTGTCTGAAGTGGCTTCTAAAA 252
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    6114 AATTAGAAGATCATTTTGAAAACATGGGAGCAAAATTGGTGTCTGAAGTGGCTTCTAAAA 6055

Qy     253 CCAATGATATTGCTGGTGATGGGACGACTACTGCAACAGTTTTGACACAAGCCATTGTTC 312
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    6054 CCAATGATATTGCTGGTGATGGGACGACTACTGCAACAGTTTTGACACAAGCCATTGTTC 5995

Qy     313 ATGAAGGACTAAAAAATGTGACAGCAGGTGCTAATCCAATTGGTATCCGTCGAGGCATTG 372
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5994 ATGAAGGACTAAAAAATGTGACAGCAGGTGCTAATCCAATTGGTATCCGTCGAGGCATTG 5935

Qy     373 AAACAGCAACAGCAACAGCTGTTGAAGCCTTGAAAGCCATTGCTCAACCTGTATCTGGCA 432
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5934 AAACAGCAACAGCAACAGCTGTTGAAGCCTTGAAAGCCATTGCTCAACCTGTATCTGGCA 5875

Qy     433 AGGAAGCTATTGCTCAGGTCGCTGCAGTATCATCACGCTCTGAAAAAGTTGGAGAGTATA 492
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5874 AGGAAGCTATTGCTCAGGTCGCTGCAGTATCATCACGCTCTGAAAAAGTTGGAGAGTATA 5815

Qy     493 TCTCAGAAGCTATGGAGCGTGTGGGCAACGATGGTGTGATTACCATCGAAGAATCTCGAG 552
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5814 TCTCAGAAGCTATGGAGCGTGTGGGCAACGATGGTGTGATTACCATCGAAGAATCTCGAG 5755

Qy     553 GTATGGAAACAGAACTTGAAGTGGTTGAAGGCATGCAATTTGACCGTGGTTACCTGTCTC 612
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5754 GTATGGAAACAGAACTTGAAGTGGTTGAAGGCATGCAATTTGACCGTGGTTACCTGTCTC 5695

Qy     613 AATACATGGTCACAGACAATGAAAAAATGGTTGCAGACCTTGAAAACCCATTTATCTTAA 672
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5694 AATACATGGTCACAGACAATGAAAAAATGGTTGCAGACCTTGAAAACCCATTTATCTTAA 5635

Qy     673 TCACGGATAAAAAAGTGTCAAACATCCAAGACATTTTGCCACTACTTGAGGAAGTTCTTA 732
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5634 TCACGGATAAAAAAGTGTCAAACATCCAAGACATTTTGCCACTACTTGAGGAAGTTCTTA 5575

Qy     733 AAACCAACCGTCCATTACTCATTATTGCAGATGATGTGGATGGTGAAGCACTTCCAACCC 792
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5574 AAACCAACCGTCCATTACTCATTATTGCAGATGATGTGGATGGTGAAGCACTTCCAACCC 5515

Qy     793 TTGTCTTGAACAAGATTCGTGGTACTTTCAATGTGGTTGCTGTCAAAGCGCCAGGATTTG 852
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5514 TTGTCTTGAACAAGATTCGTGGTACTTTCAATGTGGTTGCTGTCAAAGCGCCAGGATTTG 5455

Qy     853 GTGATCGTCGTAAAGCTATGCTTGAAGACATTGCTATCTTGACAGGTGGTACAGTGATTA 912
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5454 GTGATCGTCGTAAAGCTATGCTTGAAGACATTGCTATCTTGACAGGTGGTACAGTGATTA 5395

Qy     913 CAGAGGATCTAGGACTTGAATTAAAAGATGCTACAATGACAGCCCTTGGACAGGCTGCTA 972
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5394 CAGAGGATCTAGGACTTGAATTAAAAGATGCTACAATGACAGCCCTTGGACAGGCTGCTA 5335

Qy     973 AGATTACAGTTGATAAAGATAGCACAGTAATTGTTGAAGGTTCAGGAAGTTCAGAAGCTA 1032
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5334 AGATTACAGTTGATAAAGATAGCACAGTAATTGTTGAAGGTTCAGGAAGTTCAGAAGCTA 5275

Qy    1033 TTGCTAACCGTATTGCACTGATTAAATCGCAATTAGAAACAACAACTTCTGACTTTGACC 1092
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5274 TTGCTAACCGTATTGCACTGATTAAATCGCAATTAGAAACAACAACTTCTGACTTTGACC 5215

Qy    1093 GTGAAAAACTACAAGAACGTTTGGCGAAATTAGCTGGTGGTGTAGCTGTTATCAAAGTAG 1152
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5214 GTGAAAAACTACAAGAACGTTTGGCGAAATTAGCTGGTGGTGTAGCTGTTATCAAAGTAG 5155

Qy    1153 GAGCTCCAACAGAGACAGCTTTAAAAGAAATGAAACTTCGCATTGAGGATGCTCTAAATG 1212
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5154 GAGCTCCAACAGAGACAGCTTTAAAAGAAATGAAACTTCGCATTGAGGATGCTCTAAATG 5095

Qy    1213 CTACACGTGCAGCCGTTGAAGAAGGTATCGTTGCTGGTGGTGGAACAGCACTTATTACGG 1272
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5094 CTACACGTGCAGCCGTTGAAGAAGGTATCGTTGCTGGTGGTGGAACAGCACTTATTACGG 5035

Qy    1273 TTATTGAAAAAGTAGCAGCTCTTGAGCTTGAGGGCGATGATGCTACTGGACGTAACATTG 1332
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5034 TTATTGAAAAAGTAGCAGCTCTTGAGCTTGAGGGCGATGATGCTACTGGACGTAACATTG 4975

Qy    1333 TGCTTCGTGCTCTAGAAGAGCCTGTACGTCAAATTGCTTTAAATGCTGGGTACGAAGGCT 1392
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4974 TGCTTCGTGCTCTAGAAGAGCCTGTACGTCAAATTGCTTTAAATGCTGGGTACGAAGGCT 4915

Qy    1393 CCGTAGTTATTGACAAGTTGAAAAACAGCCCTGCAGGAACAGGATTTAATGCTGCAACAG 1452
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4914 CCGTAGTTATTGACAAGTTGAAAAACAGCCCTGCAGGAACAGGATTTAATGCTGCAACAG 4855

Qy    1453 GTGAGTGGGTTGATATGATTAAAACAGGAATCATTGACCCTGTCAAAGTAACACGATCAG 1512
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4854 GTGAGTGGGTTGATATGATTAAAACAGGAATCATTGACCCTGTCAAAGTAACACGATCAG 4795

Qy    1513 CGCTTCAAAATGCAGCTTCTGTAGCTAGTCTTATTTTGACAACAGAAGCAGTTGTTGCTA 1572
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4794 CGCTTCAAAATGCAGCTTCTGTAGCTAGTCTTATTTTGACAACAGAAGCAGTTGTTGCTA 4735

Qy    1573 ATAAACCTGAACCAGCTACGCCAGCGCCAGCAATGCCAGCAGGTATGGATCCAGGAATGA 1632
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4734 ATAAACCTGAACCAGCTACGCCAGCGCCAGCAATGCCAGCAGGTATGGATCCAGGAATGA 4675

Qy    1633 TGGGTGG 1639
           |||| ||
Db    4674 TGGGCGG 4668

RESULT 2
```

```
AE014170/c
LOCUS       AE014170               53291 bp    DNA     linear   BCT 19-JUL-2002
DEFINITION  Streptococcus pyogenes MGAS315, section 35 of 37 of the complete
            genome.
ACCESSION   AE014170 AE014074
VERSION     AE014170.1  GI:21905475
KEYWORDS    .
SOURCE      Streptococcus pyogenes MGAS315.
  ORGANISM  Streptococcus pyogenes MGAS315
            Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
            Streptococcus.
REFERENCE   1  (bases 1 to 53291)
  AUTHORS   Beres,S.B., Sylva,G.L., Barbian,K.D., Lei,B., Hoff,J.S.,
            Mammarella,N.D., Liu,M.-Y., Smoot,J.C., Porcella,S.F.,
            Parkins,L.D., McCormick,J.K., Leung,D.Y.M., Schlievert,P.M. and
            Musser,J.M.
  TITLE     Genome sequence of a serotype M3 strain of group A Streptococcus:
            Phage-encoded toxins, the high-virulence phenotype, and clone
            emergence
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (15), 10078-10083 (2002)
REFERENCE   2  (bases 1 to 53291)
  AUTHORS   Beres,S.B., Sylva,G.L., Barbian,K.D., Lei,B., Hoff,J.S.,
            Mammarella,N.D., Liu,M.-Y., Smoot,J.C., Porcella,S.F.,
            Parkins,L.D., McCormick,J.K., Leung,D.Y.M., Schlievert,P.M. and
            Musser,J.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-JUN-2002) Laboratory of Human-Bacterial Pathogenesis,
            Rocky Mountain Laboratories, NIAID, NIH, 903 South Fourth St.,
            Hamilton, MT 59840, USA
FEATURES             Location/Qualifiers
     source          1. .53291
                     /organism="Streptococcus pyogenes MGAS315"
                     /strain="MGAS315"
                     /serotype="M3"
                     /db_xref="taxon:198466"
                     /note="group: A"
     gene            complement(162. .3671)
                     /gene="scpA"
                     /note="SpyM3_1726"
     CDS             complement(162. .3671)
                     /gene="scpA"
                     /note="best blastp hit: sp|P15926|SCA1_STRPY C5A peptidase
                     precursor (SCP)"
                     /codon_start=1
                     /transl_table=11
                     /product="C5A peptidase precursor"
                     /protein_id="AAM80333.1"
                     /db_xref="GI:21905476"
                     /translation="MRKKQKLPFDKLAIALMSTSILLNAQSDIKANTVTEDTPATEQA
                     VEVPQQTAVSEEAPSSSSKETNPPQTPDDAEETVADKANDLAPQAPAKTADIPATSKE
                     TIRDLNDPSHVKTLQEKAGKGAGTVVAVIDAGFDKNHEAWRLTDKSKARYQSKEDLEK
                     AKKDHGITYGEWVNDKVAYYHDYSKDGKTAVDQEHGTHVSGILSGNAPSETKEPYRLE
                     GAMPEAQLLLMRVEIVNGLADYARNYAQAIRDAVNLGAKVINMSFGNAALAYANLPDE
                     TKKAFDYAKSKGVSIVTSAGNDSSFGGKTRLPLADHPDYGVVGTPAAADSTLTVASYS
                     PDKQLTETATVKTADQQDKEMPVLSTNRFEPNKAYDYAYANRGTKEDDFKDVKGKIAL
                     IERGDIDFKDKIANAKKAGAVGVLIYDNQDKGFPIELPNVDQMPAAFISRKDGLLLKD
                     NSKKTITFNATPKVLPTASGTKLSRFSSWGLTADGNIKPDIAAPGQDILSSVANNKYA
                     KLSGTSMSAPLVAGIMGLLQKQYETQYPDMTPSERLDLAKKVLMSSATALYDEDEKAY
                     FSPRQQGAGAVDAKKASAATMYVTDKDNTSSKVHLNNVSDKFEVTVTVHNKSDKPQEL
                     YYQATVQTDKVDGKHFALAPKALYETSWQKITIPANSSKQVTVPIDASRFSKDLLAQM
                     KNGYFLEGFVRFKQDPTKEELMSIPYIGFRGDFGNLSALEKPIYDSKDGSSYYHEANS
                     DAKDQLDGDGLQFYALKNNFTALTTESNPWTIIKAVKEGVENIEDIESSEITETIFAG
                     TFAKQDDDSHYYIHRHANGKPYAAISPNGDGNRDYVQFQGTFLRNAKNLVAEVLDKEG
                     DVVWTSEVTEQVVKNYNNDLASTLGSTRFEKTRWDGKDKDGKVVANGTYTYRVRYTPI
                     SSGAKEQHTDFDVIVDNTTPEAATSATFSAEDRRLTLASKPKTSQPVYRERIAYTYMD
                     EDLPTTEYISPNEDGTFTLPEEAETMEGATVPLKMSDFTYVVEDMAGNITYTPVTNLL
                     EGHSNKPEQDGSDQVPDKTPETKPEQDGSGQAPDKKPEAKPEQDGSGQAPDKKPETKP
                     EKDSSGQTPGKTPQKGQPSRTLEKRSSKRALATKASARDQLPTTNDKDTNRLHLLKLV
                     MTTFFFGLVAHIFKTKRQKETKK"
     gene            complement(4041. .5786)
                     /gene="emm3"
                     /note="SpyM3_1727"
     CDS             complement(4041. .5786)
                     /gene="emm3"
                     /note="best blastp hit: emb|CAA56449.1| (X80168) M3
                     protein [Streptococcus pyogenes]"
                     /codon_start=1
                     /transl_table=11
                     /product="antiphagocytic M protein, type 3"
                     /protein_id="AAM80334.1"
                     /db_xref="GI:21905477"
                     /translation="MAKNNTNRHYSLRKLKTGTASVAVALTVLGTGLVAGQTVKADAR
                     SVNGEFPRHVKLKNEIENLLDQVTQLYTKHNSNYQQYNAQAGRLDLRQKAEYLKGLND
                     WAERLLQELNGEDVKKVLGKVAFEKDDLEKEVKELKEKIDKKEKEYQDLDKDFDLAKQ
                     GYVLSDKRHQQELEEKEKKVTEATAKVGQISEELETVKQKVESTMQDLTEKQNRVSQL
                     EQELATTKQNAKEDFELAALANAADKQKLEAKIADLETKLKEAKEDFELAALGHQHAH
                     NEYQAKLAEKDDQIKQLEEQKQILDASRKGTARDLEAVRQAKKATEAELNNLKAELAK
                     VTEQKQILDASRKGTARDLEAVRQAKAQVEAALKQLEEQNRISEASRKGLRRDLDASR
                     EAKKQVEKDLANLTAELDKVKEEKQISDASRQGLRRDLDASREAKKQVEKALEEANSK
                     LAALEKLNKELEESKKLTEKEKAELQAKLEAEAKALKEQLAKQAEELAKLRAGKASDS
                     QIPDTKPGNKAVPGKGQAPQAGTKPNQNKAPMKETKRQLPSTGETANPFFTAAALTVM
                     ATAGVAAVVKRKEEN"
     gene            complement(5970. .7580)
                     /gene="mga"
                     /note="SpyM3_1728"
     CDS             complement(5970. .7580)
                     /gene="mga"
                     /note="best blastp hit: gb|AAA26931.1| (M58461) M protein
                     trans-acting positive regulator [Streptococcus pyogenes]"
                     /codon_start=1
                     /transl_table=11
                     /product="M protein trans-acting positive regulator,
                     multi-gene activator"
                     /protein_id="AAM80335.1"
                     /db_xref="GI:21905478"
                     /translation="MYVSKLFTSQQWRELKLISYVTENADAIGVKDKELSKALNISML
                     TLQTCLTNMQFMKEVGGITYKNGYITIWYHQHCGLQEVYQKALRHSQSFKLLETLFFR
                     DFNSLEELAEELFVSLSTLKRLIKKTNAYLMHTFGITILTSPVQVSGDEHQIRLFYLK
                     YFSEAYKISEWPFGEILNLKNCERLLSLMIKEVDVRVNFTLFQHLKILSSVNLIRYYK
                     GHSAVYDNKKTSHRFSQLIQSSLEIQDLSRLFYLKFGLYLDETTIAEMFSNHVNDQLE
                     IGYAFDSIKQDSPTGCRKVTNWVHLTNWVHLLDELEIRLNLSVTNKYEVAVILHNTTV
                     LKEEDITANYLFFDYKKSYLNFYKQEHPHLYKAFVAGVEKLMRSEKEPISTELTNQLI
                     YAFFITWENSFLEVNQKDEKIRLLVIERSFNSVGNFLKKYIGEFFSITNFNELDALTI
                     DLEEIEKQYDVIVTDVMVGKSDELEIFFFYKMIPEAIIDKLNAFLNISSADSLPLDKP
                     IKNPLDFHRKEVIFPTPPNKLHAPPSTS"
     gene            7968. .8162
                     /gene="SpyM3_1729"
     CDS             7968. .8162
                     /gene="SpyM3_1729"
                     /note="best blastp hit: gb|AAF99701.1|AF276241_1
                     (AF276241) aminopeptidase-N [Epiphyas postvittana]"
                     /codon_start=1
                     /transl_table=11
                     /product="hypothetical protein"
                     /protein_id="AAM80336.1"
                     /db_xref="GI:21905479"
                     /translation="MTVMVQPLKILSYFSQFTPTLALENVSTMFFMNWLTCLFSLAVL
                     RKQGFGVYFAFNFSHVTLTS"
     gene            complement(8268. .8519)
                     /gene="SpyM3_1730"
     CDS             complement(8268. .8519)
                     /gene="SpyM3_1730"
                     /note="best blastp hit: gb|AAK34696.1| (AE006624)
                     hypothetical protein (mga-associated) [Streptococcus
                     pyogenes M1 GAS], and gb|AAL98548.1| (AE010111)
                     hypothetical protein [Streptococcus pyogenes MGAS8232]"
                     /codon_start=1
                     /transl_table=11
                     /product="hypothetical protein"
                     /protein_id="AAM80337.1"
                     /db_xref="GI:21905480"
                     /translation="MIKKVTTPSQKTKKRVRNGYLLKLGTACLLLSILSYGIGLLGQP
                     SMENTFMGIASVAMLGSVCFFIIFALNRIFDALEDNLRD"
     gene            complement(8597. .10225)
                     /gene="isp.1"
                     /note="SpyM3_1731"
```

```
     CDS             complement(8597. .10225)
                     /gene="isp.1"
                     /note="best blastp hit: gb|AAK34697.1| (AE006624)
                     immunogenic secreted protein precursor [Streptococcus
                     pyogenes M1 GAS]"
                     /codon_start=1
                     /transl_table=11
                     /product="immunogenic secreted protein precursor"
                     /protein_id="AAM80338.1"
                     /db_xref="GI:21905481"
                     /translation="MKKRKLLAVTLLSTILLNSAVPLVVADTSLRNSTSSTDQPTTAD
                     TDTDDESETAKKDKKSKETASQHDTQKDHKPSHNHPTPPSNDTKQTDQASSEATDKPN
                     KDKNDTKQPNSSDQSTPSPKDQSSQKESQNKDGRPTPSPDQQKDQTPDKTPEKSADKT
                     PEKGPEKATEKTPEPNRDAPKPIQPPLAAAAPVFAPWRESDKDLSKLKPSSRSSAAYV
                     RHWTGDSAYTHNLLSRRYGITAEQLDGFLNSLGIHYDKERLNGKRLLEWEKLTGLDVR
                     AIVAIAMAESSLGTQGVAKEKGANMFGYGAFDFNPNNAKKYSDEVAIRHMVEDTIIAN
                     KNQTFERQDLKAKKWSLGQLDTLIDGGVYFTDTSGSGQRRADIMTKLDQWIDDHGSTP
                     EIPEHLKITSGTQFSEVPVGYKRSQPQNVLTYKSETYSFGQCTWYAYNRVKELGYQVD
                     RYMGNGGDWQRKPGFVTTHKPKVGYVVSFAPGQAGADATYGHVAVVEQIKEDGSILIS
                     ESNVMGLGTISYRTFTAEQASLLTYVVGDKLPRP"
     gene            complement(10327. .11715)
                     /gene="SpyM3_1732"
     CDS             complement(10327. .11715)
                     /gene="SpyM3_1732"
                     /note="best blastp hit: gb|AAK34698.1| (AE006624) putative
                     histidine kinase [Streptococcus pyogenes M1 GAS]; similar
                     to two-component sensor histidine kinase"
                     /codon_start=1
                     /transl_table=11
                     /product="putative histidine kinase"
                     /protein_id="AAM80339.1"
                     /db_xref="GI:21905482"
                     /translation="MRLIKKTFLVINGLIIVVVTSILLVLYFAMPIYYTKVKDKEVKC
                     EFDQTSKQIKGKTVTEIRDILTKKINKDNIWYSLVDSDNQLLYPSLQLLDGVSESKDS
                     QNVNIVTTFDNSYSNVKVMSQKVTLRDGKKMTLLGQSSLQPVTDASKVLLDLYPSLLI
                     FSVTVGSIVAYLYSRTSSRRILSMSQTAKKMVNLEPNLTCTIHGKDEIAMLASDINRL
                     YASLSTSIKSLQKEYEKASDSEREKSEFLRMTSHELKTPITSVIGMIDGMLYNVGDFA
                     DRDKYLRKCRDVLEGQAQLVQSILSLSKIETLASQNQELFSLKSSLEEEMEVFLVLSE
                     LKHLKVTINLEEQFVKANKVYLLKAIKNIIDNAFHYTKSGGQVMIQLKDNQLVIKNEA
                     ETLLTQQQMKQLFQPFYRPDYSRNRKDGGTGLGLFITHQILDQHHLAYRFVVLDQRWM
                     VFTIDFPSHHDD"
     gene            complement(11712. .12365)
                     /gene="SpyM3_1733"
     CDS             complement(11712. .12365)
                     /gene="SpyM3_1733"
                     /note="best blastp hit: gb|AAK34699.1| (AE006624) putative
                     two-component response regulator [Streptococcus pyogenes
                     M1 GAS], and gb|AAL98551.1| (AE010111) putative
                     two-component response regulator [Streptococcus pyogenes
                     MGAS8232]"
                     /codon_start=1
                     /transl_table=11
                     /product="putative two-component response regulator"
                     /protein_id="AAM80340.1"
                     /db_xref="GI:21905483"

  Query Match            96.8%;  Score 1607.8;  DB 1;  Length 53291;
  Best Local Similarity  99.3%;  Pred. No. 0;
  Matches 1615;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy      13 ATATGGCAAAAGAAATCAAATTTTCAGCAGATGCGCGTGCTGCCATGGTGCGCGGAGTTG 72
           |||||||||||||| || ||||||||||||||||||||||||||||||||||||||||||
Db   44887 ATATGGCAAAAGATATTAAATTTTCAGCAGATGCGCGTGCTGCCATGGTGCGCGGAGTTG 44828

Qy      73 ATATGTTAGCAGATACCGTCAAAGTAACGCTTGGTCCTAAAGGGCGCAATGTTGTTCTTG 132
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   44827 ATATGTTAGCAGATACCGTCAAAGTAACGCTTGGTCCTAAAGGGCGCAATGTTGTTCTTG 44768

Qy     133 AAAAAGCTTTTGGTTCTCCCTTAATTACTAATGACGGGGTAACCATTGCTAAAGAGATCG 192
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   44767 AAAAAGCTTTTGGTTCTCCCTTAATTACTAATGACGGGGTAACCATTGCTAAAGAGATCG 44708

Qy     193 AATTAGAAGATCATTTTGAAAACATGGGAGCAAAATTGGTGTCTGAAGTGGCTTCTAAAA 252
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   44707 AATTAGAAGATCATTTTGAAAACATGGGAGCAAAATTGGTGTCTGAAGTGGCTTCTAAAA 44648

Qy     253 CCAATGATATTGCTGGTGATGGGACGACTACTGCAACAGTTTTGACACAAGCCATTGTTC 312
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   44647 CCAATGATATTGCTGGTGATGGGACGACTACTGCAACAGTTTTGACACAAGCCATTGTTC 44588

Qy     313 ATGAAGGACTAAAAAATGTGACAGCAGGTGCTAATCCAATTGGTATCCGTCGAGGCATTG 372
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   44587 ATGAAGGACTAAAAAATGTGACAGCAGGTGCTAATCCAATTGGTATCCGTCGAGGCATTG 44528

Qy     373 AAACAGCAACAGCAACAGCTGTTGAAGCCTTGAAAGCCATTGCTCAACCTGTATCTGGCA 432
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   44527 AAACAGCAACAGCAACAGCCGTTGAAGCCTTGAAAGCCATTGCTCAACCTGTATCTGGCA 44468

Qy     433 AGGAAGCTATTGCTCAGGTCGCTGCAGTATCATCACGCTCTGAAAAAGTTGGAGAGTATA 492
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   44467 AGGAAGCTATTGCTCAGGTCGCTGCAGTATCATCACGCTCTGAAAAAGTTGGAGAGTATA 44408

Qy     493 TCTCAGAAGCTATGGAGCGTGTGGGCAACGATGGTGTGATTACCATCGAAGAATCTCGAG 552
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   44407 TCTCAGAAGCTATGGAGCGTGTGGGCAACGATGGTGTGATTACCATCGAAGAATCTCGAG 44348

Qy     553 GTATGGAAACAGAACTTGAAGTGGTTGAAGGCATGCAATTTGACCGTGGTTACCTGTCTC 612
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   44347 GTATGGAAACAGAACTTGAAGTGGTTGAAGGCATGCAATTTGACCGTGGTTACCTGTCTC 44288

Qy     613 AATACATGGTCACAGACAATGAAAAAATGGTTGCAGACCTTGAAAACCCATTTATCTTAA 672
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   44287 AATACATGGTCACAGACAATGAAAAAATGGTTGCAGACCTTGAAAACCCATTTATCTTAA 44228

Qy     673 TCACGGATAAAAAAGTGTCAAACATCCAAGACATTTTGCCACTACTTGAGGAAGTTCTTA 732
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   44227 TCACGGATAAAAAAGTGTCAAACATCCAAGACATTTTGCCACTACTTGAGGAAGTTCTTA 44168

Qy     733 AAACCAACCGTCCATTACTCATTATTGCAGATGATGTGGATGGTGAAGCACTTCCAACCC 792
           |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db   44167 AAACCAACCGTCCATTACTCATTATTGCAGATGATGTGGATGGTGAAGCCCTTCCAACCC 44108

Qy     793 TTGTCTTGAACAAGATTCGTGGTACTTTCAATGTGGTTGCTGTCAAAGCGCCAGGATTTG 852
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   44107 TTGTCTTGAACAAGATTCGTGGTACTTTCAATGTGGTTGCTGTCAAAGCGCCAGGATTTG 44048

Qy     853 GTGATCGTCGTAAAGCTATGCTTGAAGACATTGCTATCTTGACAGGTGGTACAGTGATTA 912
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   44047 GTGATCGTCGTAAAGCTATGCTTGAAGACATTGCTATCTTGACAGGTGGTACAGTGATTA 43988

Qy     913 CAGAGGATCTAGGACTTGAATTAAAAGATGCTACAATGACAGCCCTTGGACAGGCTGCTA 972
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   43987 CAGAGGATCTAGGACTTGAATTAAAAGATGCTACAATGACAGCCCTTGGACAGGCTGCTA 43928

Qy     973 AGATTACAGTTGATAAAGATAGCACAGTAATTGTTGAAGGTTCAGGAAGTTCAGAAGCTA 1032
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   43927 AGATTACAGTTGATAAAGATAGCACAGTAATTGTTGAAGGTTCAGGAAGTTCAGAAGCTA 43868

Qy    1033 TTGCTAACCGTATTGCACTGATTAAATCGCAATTAGAAACAACAACTTCTGACTTTGACC 1092
           |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db   43867 TTGCTAACCGTATTGCACTGATTAAATCGCAATTAGAGACAACAACTTCTGACTTTGACC 43808

Qy    1093 GTGAAAAACTACAAGAACGTTTGGCGAAATTAGCTGGTGGTGTAGCTGTTATCAAAGTAG 1152
           |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db   43807 GTGAAAAACTACAAGAACGTTTGGCGAAATTAGGTGGTGGTGTAGCTGTTATCAAAGTAG 43748

Qy    1153 GAGCTCCAACAGAGACAGCTTTAAAAGAAATGAAACTTCGCATTGAGGATGCTCTAAATG 1212
           |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db   43747 GAGCTCCAACAGAGACAGCTTTAAAAGAAATGAAACTTCGCATTGAGGACGCTCTAAATG 43688

Qy    1213 CTACACGTGCAGCCGTTGAAGAAGGTATCGTTGCTGGTGGTGGAACAGCACTTATTACGG 1272
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   43687 CTACACGTGCAGCCGTTGAAGAAGGTATCGTTGCTGGTGGTGGAACAGCACTTATTACGG 43628

Qy    1273 TTATTGAAAAAGTAGCAGCTCTTGAGCTTGAGGGCGATGATGCTACTGGACGTAACATTG 1332
           |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
```

```
Db  43627 TTATTGAAAAAGTAGCAGCTCTTGAACTTGAGGGCGATGATGCTACTGGACGTAACATTG 43568

Qy   1333 TGCTTCGTGCTCTAGAAGAGCCTGTACGTCAAATTGCTTTAAATGCTGGGTACGAAGGCT 1392
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  43567 TGCTTCGTGCTCTAGAAGAGCCTGTACGTCAAATTGCTTTAAATGCTGGGTACGAAGGCT 43508

Qy   1393 CCGTAGTTATTGACAAGTTGAAAAACAGCCCTGCAGGAACAGGATTTAATGCTGCAACAG 1452
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  43507 CCGTAGTTATTGACAAGTTGAAAAACAGCCCTGCAGGAACAGGATTTAATGCTGCAACAG 43448

Qy   1453 GTGAGTGGGTTGATATGATTAAAACAGGAATCATTGACCCTGTCAAAGTAACACGATCAG 1512
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  43447 GTGAGTGGGTTGATATGATTAAAACAGGAATCATTGACCCTGTCAAAGTAACACGATCAG 43388

Qy   1513 CGCTTCAAAATGCAGCTTCTGTAGCTAGTCTTATTTTGACAACAGAAGCAGTTGTTGCTA 1572
          |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db  43387 CGCTTCAAAATGCAGCTTCTGTAGCTAGTCTGATTTTGACAACAGAAGCAGTTGTTGCTA 43328

Qy   1573 ATAAACCTGAACCAGCTACGCCAGCGCCAGCAATGCCAGCAGGTATGGATCCAGGAATGA 1632
          |||| ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db  43327 ATAAGCCTGAACCAGCTGCGCCAGCGCCAGCAATGCCAGCAGGTATGGATCCAGGAATGA 43268

Qy   1633 TGGGTGG 1639
          |||| ||
Db  43267 TGGGCGG 43261


RESULT 3
AE010115/c
LOCUS       AE010115               11576 bp    DNA     linear   BCT 03-APR-2002
DEFINITION  Streptococcus pyogenes strain MGAS8232, section 163 of 173 of the
            complete genome.
ACCESSION   AE010115 AE009949
VERSION     AE010115.1  GI:19749196
KEYWORDS    .
SOURCE      Streptococcus pyogenes MGAS8232.
  ORGANISM  Streptococcus pyogenes MGAS8232
            Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
            Streptococcus.
REFERENCE   1  (bases 1 to 11576)
  AUTHORS   Smoot,J.C., Barbian,K.D., Van Gompel,J.J., Smoot,L.M.,
            Chaussee,M.S., Sylva,G.L., Sturdevant,D.E., Ricklefs,S.M.,
            Porcella,S.F., Parkins,L.D., Beres,S.B., Campbell,D.S., Smith,T.M.,
            Zhang,Q., Kapur,V., Daly,J.A., Veasy,L.G. and Musser,J.M.
  TITLE     Genome sequence and comparative microarray analysis of serotype M18
            group A Streptococcus strains associated with acute rheumatic fever
            outbreaks
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (7), 4668-4673 (2002)
  MEDLINE   21927593
   PUBMED   11917108
REFERENCE   2  (bases 1 to 11576)
  AUTHORS   Smoot,J.C., Barbian,K.D., Van Gompel,J.J., Smoot,L.M.,
            Chaussee,M.S., Sylva,G.L., Sturdevant,D.E., Ricklefs,S.M.,
            Porcella,S.F., Parkins,L.D., Beres,S.B., Campbell,D.S., Smith,T.M.,
            Zhang,Q., Kapur,V., Daly,J.A., Veasy,L.George. and Musser,J.M.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JAN-2002) Laboratory of Human Bacterial
            Pathogenesis/Rocky Mountain Laboratories/NIAID/NIH, 903 S. 4th St.,
            Hamilton, MT 59840, USA
FEATURES             Location/Qualifiers.
     source          1. .11576
                     /organism="Streptococcus pyogenes MGAS8232"
                     /strain="MGAS8232"
                     /db_xref="taxon:186103"
     misc_feature    complement(38. .283)
                     /note="spyM18_2128; probable gene fragment; best blastp
                     match dbj|BAA95200.1| (AB025228) rgg [Streptococcus
                     oralis]"
     gene            complement(535. .2166)
                     /gene="groL"
                     /note="spyM18_2129"
     CDS             complement(535. .2166)
                     /gene="groL"
                     /note="best blastp match sp|P82485|CH60_STRPY 60 KDA
                     CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN)"
                     /codon_start=1
                     /transl_table=11
                     /product="heat shock protein (chaperonin)"
                     /protein_id="AAL98581.1"
                     /db_xref="GI:19749197"
                     /translation="MAKDIKFSADARAAMVRGVDMLADTVKVTLGPKGRNVVLEKAFG
                     SPLITNDGVTIAKEIELEDHFENMGAKLVSEVASKTNDIAGDGTTTATVLTQAIVHEG
                     LKNVTAGANPIGIRRGIETATATAVEALKAIAQPVSGKEAIAQVAAVSSRSEKVGEYI
                     SEAMERVGNDGVITIEESRGMETELEVVEGMQFDRGYLSQYMVTDNEKMVADLENPFI
                     LITDKKVSNIQDILPLLEEVLKTNRPLLIIADDVDGEALPTLVLNKIRGTFNVVAVKA
                     PGFGDRRKAMLEDIAILTGGTVITEDLGLELKDATMTALGQAAKITVDKDSTVIVEGS
                     GSSEAIANRIALIKSQLETTTSDFDREKLQERLAKLAGGVAVIKVGAPTETALKEMKL
                     RIEDALNATRAAVEEGIVAGGGTALITVIEKVAALELEGDDATGRNIVLRALEEPVRQ
                     IALNAGYEGSVIIDKLKNSPAGTGFNAATGEWVDMIKTGIIDPVKVTRSALQNAASVA
                     SLILTTEAVVANKPEPAAPAPAMPAGMDPGMMGGF"
     gene            complement(2202. .2492)
                     /gene="groS"
                     /note="spyM18_2131"
     CDS             complement(2202. .2492)
                     /gene="groS"
                     /note="best blastp match gb|AAK34728.1| (AE006627) heat
                     shock protein - cochaperonin [Streptococcus pyogenes M1
                     GAS]"
                     /codon_start=1
                     /transl_table=11
                     /product="heat shock protein - cochaperonin"
                     /protein_id="AAL98582.1"
                     /db_xref="GI:19749198"
                     /translation="MLKPLGDRVVVRFDDEKEQTVGGFVLAGTHKESTRKATVLAVSE
                     TGVRTITGDSVLPSVSVGQEVLVENGHDLEVTVDDEKVSIIRESDIIAIVTK"
     gene            2740. .3582
                     /gene="tra"
                     /note="spyM18_2133"
     CDS             2740. .3582
                     /gene="tra"
                     /note="best blastp match gb|AAA59388.1| (U11799) putative
                     transposase [Streptococcus pyogenes]"
                     /codon_start=1
                     /transl_table=11
                     /product="putative transposase"
                     /protein_id="AAL98583.1"
                     /db_xref="GI:19749199"
                     /translation="MQDYYTPKGKQLTIHERRQIQRWKLEGRSNREIARLLGKAPQTI
                     HNEIKRGLVRQQVRKGKFEAVYSAQHAQLVYQENRKRSVRPIRQRKQDREAIEHYMRQ
                     NYSPEMIVKAKGVQVPVSTIYYWIHHGKLSLGKEAMLYPRKAKQARKHASPYFKPAGK
                     SIEQRPDSINQRLEAGHYEIDTVILTRAKNQCLLTLTDRKTRHQLIRLIPDKSAQAVN
                     KALTGILKDYTVNSITADNGTEFSRLSDVSLKVPKQRPLKKSLLLNIGSIIILNDSST
                     TSRQ"
     gene            complement(3665. .6109)
                     /gene="clp"
                     /note="spyM18_2134"
     CDS             complement(3665. .6109)
                     /gene="clp"
                     /note="best blastp match gb|AAK34729.1| (AE006627)
                     putative endopeptidase Clp ATP-binding chain C
                     [Streptococcus pyogenes M1 GAS]"
                     /codon_start=1
                     /transl_table=11
                     /product="putative endopeptidase Clp ATP-binding chain C"
                     /protein_id="AAL98584.1"
                     /db_xref="GI:19749200"
                     /translation="MIMYSTKMQDIFRQAQFQAARFDSHCLETWHVLLAMVAVDNSLA
                     NMILSEYDAQVAIEEYEAAAILAMGKTPKEQLSRVDFRPQSKTLTNLLAFAQAISQIT
                     RDQEVGSEHVLFAILLNPDIMASRLLEIAGYQIKDNGNGQPRLADLRKAIERHAGYSK
                     EMIKAIHELRKPKKTKTQGTFSDMMKPPSTAGELSDFTRDLTEMARQGLLESVIGRDQ
                     EVSRMIQVLSRKTKNNPVLVGDAGVGKTALAYGLAQRIANGAIPYELKEMRVLELDMM
                     SVVAGTRFRGDFEERMNQIIDDIEADGQIILFVDELHTIMGSGSGIDSTLDAANILKP
                     ALSRGTLHMVGATTQEEYQKHIEKDAALSRRFAKILIEEPNTEDAYQILMGLKLSYET
                     YHNVSISNEAVKTAVKMAHRYLTSKNLPDSAIDLLDEASAAVQNMVKKSAPETLTPID
                     QALINGDMKKVSRLLAKEAKGQMRKPTPVTEDDILATLSKLSGIPLEKLTQADSKKYL
                     NLEKELHKRVIGQDAAVTAISRAIRRNQSGIRTGKRPIGSFMFLGPTGVGKTELAKAL
```

```
                AEVLFDDEAALIRFDMSEYMEKFAASRLNGAPPGYVGYDEGGELTQKVRNKPYSVLLF
                DEVEKAHPDIFNVLLQVLDDGILTDSRGRKVDFSNTIIIMTSNLGATALRDDKTVGFG
                VKGIHQDHQAMEKRILEELRKTYRPEFINRIDEKVVFHSLTQDNMRDVVKIMVQPLIT
                TLAEKGITLKIQPLALKHLSEVGYDEHMGARPLRRTLQTEIEDKLSELILSRELTSGH
                TLKIGLSYGKLTFHIA"
gene            complement(6109. .6570)
                /gene="spyM18_2135"
CDS             complement(6109. .6570)
                /gene="spyM18_2135"
                /note="best blastp match gb|AAK34730.1| (AE006627)
                putative transcriptional regulator [Streptococcus pyogenes
                M1 GAS]"
                /codon_start=1
                /transl_table=11
                /product="putative transcriptional regulator"
                /protein_id="AAL98585.1"
                /db_xref="GI:19749201"
                /translation="MPTKNTSDSIEEYIKELLAKSGIAEIKRSMLADSFQVVPSQINY
                VIKTRFTESRGYEVESKRGGGGYIRIAKVHFSDKHHLIGNLMATIEDCISEQVFTDSI
                QLLFDEHLLTEREGNIILAVASDDVLGTDGSTIRARMLYRLLQRIDRKGSN"
gene            complement(6766. .6969)
                /gene="cspC"
                /note="spyM18_2136"
CDS             complement(6766. .6969)
                /gene="cspC"
                /note="best blastp match sp|Q54974|CSPA_STRPY MAJOR
                COLD-SHOCK PROTEIN"
                /codon_start=1
                /transl_table=11
                /product="putative cold shock protein"
                /protein_id="AAL98586.1"
                /db_xref="GI:19749202"
                /translation="MAQGTVKWFNAEKGFGFISTENGQDVFAHFSAIQTNGFKTLEEG
                QKVAFDVEEGQRGPQAVNITKLA"
gene            7955. .8515
                /gene="ahpC"
                /note="spyM18_2137"
CDS             7955. .8515
                /gene="ahpC"
                /note="best blastp match gb|AAK34732.1| (AE006628)
                putative alkyl hydroperoxidase [Streptococcus pyogenes M1
                GAS]"
                /codon_start=1
                /transl_table=11
                /product="putative alkyl hydroperoxidase"
                /protein_id="AAL98587.1"
                /db_xref="GI:19749203"
                /translation="MSLIGKEIAEFSAQAYHDGKFITVTNEDVKGKWAVFCFYPADFS
                FVCPTELGDLQEQYETLKSLGVEVYSVSTDTHFVHKAWHDDSDVVGTITYPMIGDPSH
                LISQAFEVLGEDGLAQRGTFIVDPDGIIQMMEINADGIGRDASTLIDKIHAAQYVRKH
                PGEVCPAKWKEGAETLTPSLDLVGKI"
gene            8536. .10068
                /gene="spyM18_2138"
CDS             8536. .10068
                /gene="spyM18_2138"
                /note="best blastp match gb|AAK34733.1| (AE006628)
                putative NADH oxidase/alkyl hydroperoxidase reductase
                [Streptococcus pyogenes M1 GAS]"
                /codon_start=1
                /transl_table=11
                /product="putative NADH oxidase/alkyl hydroperoxidase
                reductase"
                /protein_id="AAL98588.1"
                /db_xref="GI:19749204"
                /translation="MALSPDIKEQLAQYLTLLEADLVLQVSLGDNEQSQKVKDFVEEI
                AAMSERISIENITLDRQPSFKVAKKGHDSGVVFAGLPLGHELTSFILALLQVSGRAPK
                VDQDVIDRIKAIDRPLHFETYVSLTCHNCPDVVQALNIMSVLNDKISHTMVEGGMFQD
                EVKAKGIMSVPTVFLDGEEFTSGRATIEQLLEQIAGPLSEEAFADKGLYDVLVIGGGP
                AGNSAAIYAARKGLKTGLLAETFGGQVMETVGIENMIGTLYTEGPKLMAEVEAHTKSY
                DVDIIKAQLATSIEKKENIEVTLANGAVLQAKTAILALGAKWRNINVPGEDEFRNKGV
                TYCPHCDGPLFEGKDVAVIGGGNSGLEAALDLAGLAKHVYVLEFLPELKADKVLQDRA
                ADTANMTIIKNVATKDIVGDDHVTGLNYTERDSGEDKHLDLEGVFVQIGLVPNTAWLK
                DSGVNLTDRGEIIVDKHGSTNIPGIFAAGDCTDSAYKQIIISMGSGATAAIGAFDYLI
```

```
                RQ"
gene            complement(10126. .11412)
                /gene="hutI"
                /note="spyM18_2139"
CDS             complement(10126. .11412)
                /gene="hutI"
                /note="best blastp match sp|P58080|HUTI_STRPY
                IMIDAZOLONEPROPIONASE (IMIDAZOLONE-5-PROPIONATE
                HYDROLASE)"
                /codon_start=1
```

```
Query Match             96.6%;  Score 1604.6;  DB 1;  Length 11576;
Best Local Similarity   99.1%;  Pred. No. 0;
Matches 1613;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy      13 ATATGGCAAAAGAAATCAAATTTTCAGCAGATGCGCGTGCTGCCATGGTGCGCGGAGTTG 72
           |||||||||||||| || ||||||||||||||||||||||||||||||||||||||||||
Db    2168 ATATGGCAAAAGATATTAAATTTTCAGCAGATGCGCGTGCTGCCATGGTGCGCGGAGTTG 2109

Qy      73 ATATGTTAGCAGATACCGTCAAAGTAACGCTTGGTCCTAAAGGGCGCAATGTTGTTCTTG 132
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2108 ATATGTTAGCAGATACCGTCAAAGTAACGCTTGGTCCTAAAGGGCGCAATGTTGTTCTTG 2049

Qy     133 AAAAAGCTTTTGGTTCTCCCTTAATTACTAATGACGGGGTAACCATTGCTAAAGAGATCG 192
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2048 AAAAAGCTTTTGGTTCTCCCTTAATTACTAATGACGGGGTAACCATTGCTAAAGAGATCG 1989

Qy     193 AATTAGAAGATCATTTTGAAAACATGGGAGCAAAATTGGTGTCTGAAGTGGCTTCTAAAA 252
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1988 AATTAGAAGATCATTTTGAAAACATGGGAGCAAAATTGGTGTCTGAAGTGGCTTCTAAAA 1929

Qy     253 CCAATGATATTGCTGGTGATGGGACGACTACTGCAACAGTTTTGACACAAGCCATTGTTC 312
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1928 CCAATGATATTGCTGGTGATGGGACGACTACTGCAACAGTTTTGACACAAGCCATTGTTC 1869

Qy     313 ATGAAGGACTAAAAAATGTGACAGCAGGTGCTAATCCAATTGGTATCCGTCGAGGCATTG 372
           |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    1868 ATGAAGGACTAAAAAATGTGACAGCAGGTGCTAATCCAATTGGTATTCGTCGAGGCATTG 1809

Qy     373 AAACAGCAACAGCAACAGCTGTTGAAGCCTTGAAAGCCATTGCTCAACCTGTATCTGGCA 432
           |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db    1808 AAACAGCAACAGCAACAGCCGTTGAAGCCTTGAAAGCCATTGCTCAACCTGTATCTGGCA 1749

Qy     433 AGGAAGCTATTGCTCAGGTCGCTGCAGTATCATCACGCTCTGAAAAAGTTGGAGAGTATA 492
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1748 AGGAAGCTATTGCTCAGGTCGCTGCAGTATCATCACGCTCTGAAAAAGTTGGAGAGTATA 1689

Qy     493 TCTCAGAAGCTATGGAGCGTGTGGGCAACGATGGTGTGATTACCATCGAAGAATCTCGAG 552
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1688 TCTCAGAAGCTATGGAGCGTGTGGGCAACGATGGTGTGATTACCATCGAAGAATCTCGAG 1629

Qy     553 GTATGGAAACAGAACTTGAAGTGGTTGAAGGCATGCAATTTGACCGTGGTTACCTGTCTC 612
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1628 GTATGGAAACAGAACTTGAAGTGGTTGAAGGCATGCAATTTGACCGTGGTTACCTGTCTC 1569

Qy     613 AATACATGGTCACAGACAATGAAAAAATGGTTGCAGACCTTGAAAACCCATTTATCTTAA 672
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1568 AATACATGGTCACAGACAATGAAAAAATGGTTGCAGACCTTGAAAACCCATTTATCTTAA 1509

Qy     673 TCACGGATAAAAAAGTGTCAAACATCCAAGACATTTTGCCACTACTTGAGGAAGTTCTTA 732
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1508 TCACGGATAAAAAAGTGTCAAACATCCAAGACATTTTGCCACTACTTGAGGAAGTTCTTA 1449

Qy     733 AAACCAACCGTCCATTACTCATTATTGCAGATGATGTGGATGGTGAAGCACTTCCAACCC 792
           |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db    1448 AAACCAACCGTCCATTACTCATTATTGCAGATGATGTGGATGGTGAAGCCCTTCCAACCC 1389

Qy     793 TTGTCTTGAACAAGATTCGTGGTACTTTCAATGTGGTTGCTGTCAAAGCGCCAGGATTTG 852
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1388 TTGTCTTGAACAAGATTCGTGGTACTTTCAATGTGGTTGCTGTCAAAGCGCCAGGATTTG 1329

Qy     853 GTGATCGTCGTAAAGCTATGCTTGAAGACATTGCTATCTTGACAGGTGGTACAGTGATTA 9
           ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db   1328 GTGATCGCCGTAAAGCTATGCTTGAAGACATTGCTATCTTGACAGGTGGTACAGTGATTA 1269

Qy    913 CAGAGGATCTAGGACTTGAATTAAAAGATGCTACAATGACAGCCCTTGGACAGGCTGCTA 972
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1268 CAGAGGATCTAGGACTTGAATTAAAAGATGCTACAATGACAGCCCTTGGACAGGCTGCTA 1209

Qy    973 AGATTACAGTTGATAAAGATAGCACAGTAATTGTTGAAGGTTCAGGAAGTTCAGAAGCTA 1032
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1208 AGATTACAGTTGATAAAGATAGCACAGTAATTGTTGAAGGTTCAGGAAGTTCAGAAGCTA 1149

Qy   1033 TTGCTAACCGTATTGCACTGATTAAATCGCAATTAGAAACAACAACTTCTGACTTTGACC 1092
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1148 TTGCTAACCGTATTGCACTGATTAAATCGCAATTAGAAACAACAACTTCTGACTTTGACC 1089

Qy   1093 GTGAAAAACTACAAGAACGTTTGGCGAAATTAGCTGGTGGTGTAGCTGTTATCAAAGTAG 1152
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1088 GTGAAAAACTACAAGAACGTTTGGCGAAATTAGCTGGTGGTGTAGCTGTTATCAAAGTAG 1029

Qy   1153 GAGCTCCAACAGAGACAGCTTTAAAAGAAATGAAACTTCGCATTGAGGATGCTCTAAATG 1212
          |||||||||||||||||||||||||||||||||||| ||||||||||| ||||||||||
Db   1028 GAGCTCCAACAGAGACAGCTTTAAAAGAAATGAAACTCCGCATTGAGGACGCTCTAAATG 969

Qy   1213 CTACACGTGCAGCCGTTGAAGAAGGTATCGTTGCTGGTGGTGGAACAGCACTTATTACGG 1272
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    968 CTACACGTGCAGCCGTTGAAGAAGGTATCGTTGCTGGTGGTGGAACAGCACTTATTACGG 909

Qy   1273 TTATTGAAAAAGTAGCAGCTCTTGAGCTTGAGGGCGATGATGCTACTGGACGTAACATTG 1332
          |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db    908 TTATTGAAAAAGTAGCAGCTCTTGAACTTGAGGGCGATGATGCTACTGGACGTAACATTG 849

Qy   1333 TGCTTCGTGCTCTAGAAGAGCCTGTACGTCAAATTGCTTTAAATGCTGGGTACGAAGGCT 1392
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    848 TGCTTCGTGCTCTAGAAGAGCCTGTACGTCAAATTGCTTTAAATGCTGGGTACGAAGGCT 789

Qy   1393 CCGTAGTTATTGACAAGTTGAAAAACAGCCCTGCAGGAACAGGATTTAATGCTGCAACAG 1452
          ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    788 CCGTAATTATTGACAAGTTGAAAAACAGCCCTGCAGGAACAGGATTTAATGCTGCAACAG 729

Qy   1453 GTGAGTGGGTTGATATGATTAAAACAGGAATCATTGACCCTGTCAAAGTAACACGATCAG 1512
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    728 GTGAGTGGGTTGATATGATTAAAACAGGAATCATTGACCCTGTCAAAGTAACACGATCAG 669

Qy   1513 CGCTTCAAAATGCAGCTTCTGTAGCTAGTCTTATTTTGACAACAGAAGCAGTTGTTGCTA 1572
          |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db    668 CGCTTCAAAATGCAGCTTCTGTAGCTAGTCTTATTTTGACAACAGAAGCAGTTGTCGCTA 609

Qy   1573 ATAAACCTGAACCAGCTACGCCAGCGCCAGCAATGCCAGCAGGTATGGATCCAGGAATGA 1632
          ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db    608 ATAAACCTGAACCAGCAGCGCCAGCGCCAGCAATGCCAGCAGGTATGGATCCAGGAATGA 549

Qy   1633 TGGGTGG 1639
          |||| ||
Db    548 TGGGCGG 542
```

```
RESULT 4
SPGROELGN
LOCUS       SPGROELGN               2683 bp    DNA     linear   BCT 26-SEP-1997
DEFINITION  S.pyogenes DNA for groEL gene.
ACCESSION   X89236
VERSION     X89236.1  GI:2462691
KEYWORDS    groEL gene; heat shock protein 60 (GroEL) like protein.
SOURCE      Streptococcus pyogenes.
  ORGANISM  Streptococcus pyogenes
            Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
            Streptococcus.
REFERENCE   1  (bases 1 to 2683)
  AUTHORS   Podbielski,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-JUN-1995) A. Podbielski, Institut f Med
            Mikrobiologie, an der Rhein Westf. Techn. Hochschule, Aachen,
            Pauwelsstr Klinikum, 52057 Aachen, FRG
REFERENCE   2  (bases 1 to 2683)
  AUTHORS   Pohl,B., Podbielski,A. and Zarges,I.
  JOURNAL   Unpublished
COMMENT     Related sequences M81132, M84965.
FEATURES             Location/Qualifiers
     source          1. .2683
                     /organism="Streptococcus pyogenes"
                     /strain="serotype M49"
                     /isolate="CS101"
                     /db_xref="taxon:1314"
     gene            1. .1446
                     /gene="groEL"
     CDS             <1. .1446
                     /gene="groEL"
                     /codon_start=1
                     /transl_table=11
                     /product="heat shock protein"
                     /protein_id="CAA61520.1"
                     /db_xref="GI:2462692"
                     /db_xref="SPTREMBL:O33733"
                     /translation="DHFENMGAKLVSEVASKTNDIAGDGTTTATVLTQAIVHEGLKNV
                     TAGANPIGIRRGIETATATAVEALKAVAQPVSGKEAIAQVAAVSSRSEKVGEYISEAM
                     ERVGNDGVITIEESRGMETELEVVEGMQFDRGYLSQYMVTDNEKMVADLENPFILIMD
                     KKVSNIQDILPLLEEVLKTNRPLLIIADDVDGEALPTLVLNKIRGTFNVVAVKAPGFG
                     DRRKAMLEDIAILTGGTVITEDLGLELKDATMTALGQAAKITVDKDSTVIVEGSGSSE
                     AIANRIALIKSQLETTTSDFDREKLQERLAKLAGGVAVIKVGAPTETALKEMKLRIED
                     ALNATRAAVEEGIVAGGGTALITVIEKVAALELEGDDATGRNIVLRALEEPVRQIALN
                     AGYEGSVVIDKLKNSPAGTGFNAATGEWVDMIKTGIIDPVKVTRSALQNAASVASLIL
                     TTEAVVANKPEPAAPAPAMPAGMDPGMMGGF"
     repeat_region   1509. .1564
                     /rpt_type=INVERTED
BASE COUNT      808 a    490 c    593 g    792 t
ORIGIN
```

Query Match 85.1%; Score 1413.4; DB 1; Length 2683;
Best Local Similarity 98.9%; Pred. No. 2.3e-278;
Matches 1423; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

```
Qy    201 GATCATTTTGAAAACATGGGAGCAAAATTGGTGTCTGAAGTGGCTTCTAAAACCAATGAT 260
          |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GATCATTTCGAAAACATGGGAGCAAAATTGGTGTCTGAAGTGGCTTCTAAAACCAATGAT 60

Qy    261 ATTGCTGGTGATGGGACGACTACTGCAACAGTTTTGACACAAGCCATTGTTCATGAAGGA 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ATTGCTGGTGATGGGACGACTACTGCAACAGTTTTGACACAAGCCATTGTTCATGAAGGA 120

Qy    321 CTAAAAAAATGTGACAGCAGGTGCTAATCCAATTGGTATCCGTCGAGGCATTGAAACAGCA 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CTAAAAAAATGTGACAGCAGGTGCTAATCCAATTGGTATCCGTCGAGGCATTGAAACAGCA 180

Qy    381 ACAGCAACAGCTGTTGAAGCCTTGAAAGCCATTGCTCAACCTGTATCTGGCAAGGAAGCT 440
          |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    181 ACAGCAACAGCTGTTGAAGCCTTGAAAGCCGTTGCTCAACCTGTATCTGGCAAGGAAGCT 240

Qy    441 ATTGCTCAGGTCGCTGCAGTATCATCACGCTCTGAAAAAGTTGGAGAGTATATCTCAGAA 500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ATTGCTCAGGTCGCTGCAGTATCATCACGCTCTGAAAAAGTTGGAGAGTATATCTCAGAA 300

Qy    501 GCTATGGAGCGTGTGGGCAACGATGGTGTGATTACCATCGAAGAATCTCGAGGTATGGAA 560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GCTATGGAGCGTGTGGGCAACGATGGTGTGATTACCATCGAAGAATCTCGAGGTATGGAA 360

Qy    561 ACAGAACTTGAAGTGGTTGAAGGCATGCAATTTGACCGTGGTTACCTGTCTCAATACATG 620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ACAGAACTTGAAGTGGTTGAAGGCATGCAATTTGACCGTGGTTACCTGTCTCAATACA- 420

Qy    621 GTCACAGACAATGAAAAAATGGTTGCAGACCTTGAAAACCCATTTATCTTAATCACG 680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||| | | |
Db    421 GTCACAGACAATGAAAAAATGGTTGCAGACCTTGAAAACCCATTTATCTTAATTATC 480

Qy    681 AAAAAAGTGTCAAACATCCAAGACATTTTGCCACTACTTGAGGAAGTTCTTAAAAC 740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 AAAAAAGTGTCAAACATCCAAGACATTTTGCCACTACTTGAGGAAGTTCTTAAA- 535
```

```
Qy    741 CGTCCATTACTCATTATTGCAGATGATGTGGATGGTGAAGCACTTCCAACCCTTGTCTTG 800
          ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db    541 CGTCCATTACTCATTATTGCAGATGATGTGGATGGTGAAGCCCTTCCAACCCTTGTCTTG 600

Qy    801 AACAAGATTCGTGGTACTTTCAATGTGGTTGCTGTCAAAGCGCCAGGATTTGGTGATCGT 860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AACAAGATTCGTGGTACTTTCAATGTGGTTGCTGTCAAAGCGCCAGGATTTGGTGATCGT 660

Qy    861 CGTAAAGCTATGCTTGAAGACATTGCTATCTTGACAGGTGGTACAGTGATTACAGAGGAT 920
          |||||||||||||||||||||||||||||||||||||||| |||||||| ||||||||||||||
Db    661 CGTAAAGCTATGCTTGAAGACATTGCTATCTTGACTGGTGGTACTGTGATTACAGAGGAT 720

Qy    921 CTAGGACTTGAATTAAAAGATGCTACAATGACAGCCCTTGGACAGGCTGCTAAGATTACA 980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CTAGGACTTGAATTAAAAGATGCTACAATGACAGCCCTTGGACAGGCTGCTAAGATTACA 780

Qy    981 GTTGATAAAGATAGCACAGTAATTGTTGAAGGTTCAGGAAGTTCAGAAGCTATTGCTAAC 1040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GTTGATAAAGATAGCACAGTAATTGTTGAAGGTTCAGGAAGTTCAGAAGCTATTGCTAAC 840

Qy   1041 CGTATTGCACTGATTAAATCGCAATTAGAAACAACAACTTCTGACTTTGACCGTGAAAAA 1100
          || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CGCATTGCACTGATTAAATCGCAATTAGAAACAACAACTTCTGACTTTGACCGTGAAAAA 900

Qy   1101 CTACAAGAACGTTTGGCGAAATTAGCTGGTGGTGTAGCTGTTATCAAAGTAGGAGCTCCA 1160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CTACAAGAACGTTTGGCGAAATTAGCTGGTGGTGTAGCTGTTATCAAAGTAGGAGCTCCA 960

Qy   1161 ACAGAGACAGCTTTAAAAGAAATGAAACTTCGCATTGAGGATGCTCTAAATGCTACACGT 1220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db    961 ACAGAGACAGCTTTAAAAGAAATGAAACTTCGCATTGAGGATGCTCTAAATGCCACACGT 1020

Qy   1221 GCAGCCGTTGAAGAAGGTATCGTTGCTGGTGGTGGAACAGCACTTATTACGGTTATTGAA 1280
          |||||||||||||||||||||||||||||||||||||||||||||| || |||
Db   1021 GCAGCCGTTGAAGAAGGTATCGTTGCTGGTGGTGGAACAGCACTTATTACGGTGATCGAA 1080

Qy   1281 AAAGTAGCAGCTCTTGAGCTTGAGGGCGATGATGCTACTGGACGTAACATTGTGCTTCGT 1340
          |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 AAAGTAGCTGCTCTTGAGCTTGAGGGCGATGACGCTACTGGACGTAACATTGTGCTTCGT 1140

Qy   1341 GCTCTAGAAGAGCCTGTACGTCAAATTGCTTTAAATGCTGGGTACGAAGGCTCCGTAGTT 1400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GCTCTAGAAGAGCCTGTACGTCAAATTGCTTTAAATGCTGGGTACGAAGGCTCCGTAGTT 1200

Qy   1401 ATTGACAAGTTGAAAAACAGCCCTGCAGGAACAGGATTTAATGCTGCAACAGGTGAGTGG 1460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 ATTGACAAGTTGAAAAACAGCCCTGCAGGAACAGGATTTAATGCTGCAACAGGTGAGTGG 1260

Qy   1461 GTTGATATGATTAAAACAGGAATCATTGACCCTGTCAAAGTAACACGATCAGCGCTTCAA 1520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GTTGATATGATTAAAACAGGAATCATTGACCCTGTCAAAGTAACACGATCAGCGCTTCAA 1320

Qy   1521 AATGCAGCTTCTGTAGCTAGTCTTATTTTGACAACAGAAGCAGTTGTTGCTAATAAACCT 1580
          |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db   1321 AATGCAGCTTCTGTAGCTAGTCTTATTTTGACAACAGAAGCAGTTGTTGCTAATAAGCCT 1380

Qy   1581 GAACCAGCTACGCCAGCGCCAGCAATGCCAGCAGGTATGGATCCAGGAATGATGGGTGG 1639
          ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||| ||
Db   1381 GAACCAGCTGCGCCAGCGCCAGCAATGCCAGCAGGTATGGATCCAGGAATGATGGGCGG 1439
```

```
RESULT 5
AX148805
LOCUS       AX148805               2683 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 7 from Patent WO0136625.
ACCESSION   AX148805
VERSION     AX148805.1  GI:14347329
KEYWORDS    .
SOURCE      Streptococcus pyogenes.
  ORGANISM  Streptococcus pyogenes
            Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
            Streptococcus.
REFERENCE   1  (bases 1 to 2683)
  AUTHORS   Wright,J.A., Young,A.H. and Dugourd,D.
  TITLE     Antisense oligonucleotide sequences derived from groel and groes as
            inhibitors of microorganisms
  JOURNAL   Patent: WO 0136625-A 7 25-MAY-2001;
            GeneSense Technologies Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .2683
                     /organism="Streptococcus pyogenes"
                     /db_xref="taxon:1314"
BASE COUNT      808 a    490 c    593 g    792 t
ORIGIN
```

Query Match 85.1%; Score 1413.4; DB 6; Length 2683;
Best Local Similarity 98.9%; Pred. No. 2.3e-278;
Matches 1423; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

```
Qy    201 GATCATTTTGAAAACATGGGAGCAAAATTGGTGTCTGAAGTGGCTTCTAAAACCAATGAT 260
          |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GATCATTTCGAAAACATGGGAGCAAAATTGGTGTCTGAAGTGGCTTCTAAAACCAATGAT 60

Qy    261 ATTGCTGGTGATGGGACGACTACTGCAACAGTTTTGACACAAGCCATTGTTCATGAAGGA 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ATTGCTGGTGATGGGACGACTACTGCAACAGTTTTGACACAAGCCATTGTTCATGAAGGA 120

Qy    321 CTAAAAAATGTGACAGCAGGTGCTAATCCAATTGGTATCCGTCGAGGCATTGAAACAGCA 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CTAAAAAATGTGACAGCAGGTGCTAATCCAATTGGTATCCGTCGAGGCATTGAAACAGCA 180

Qy    381 ACAGCAACAGCTGTTGAAGCCTTGAAAGCCATTGCTCAACCTGTATCTGGCAAGGAAGCT 440
          |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db    181 ACAGCAACAGCTGTTGAAGCCTTGAAAGCCGTTGCTCAACCTGTATCTGGCAAGGAAGCT 240

Qy    441 ATTGCTCAGGTCGCTGCAGTATCATCACGCTCTGAAAAAGTTGGAGAGTATATCTCAGAA 500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ATTGCTCAGGTCGCTGCAGTATCATCACGCTCTGAAAAAGTTGGAGAGTATATCTCAGAA 300

Qy    501 GCTATGGAGCGTGTGGGCAACGATGGTGTGATTACCATCGAAGAATCTCGAGGTATGGAA 560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GCTATGGAGCGTGTGGGCAACGATGGTGTGATTACCATCGAAGAATCTCGAGGTATGGAA 360

Qy    561 ACAGAACTTGAAGTGGTTGAAGGCATGCAATTTGACCGTGGTTACCTGTCTCAATACATG 620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ACAGAACTTGAAGTGGTTGAAGGCATGCAATTTGACCGTGGTTACCTGTCTCAATACATG 420

Qy    621 GTCACAGACAATGAAAAAATGGTTGCAGACCTTGAAAACCCATTTATCTTAATCACGGAT 680
          |||||||||||||||||||||||||||||||||||||||||||||||||||| | ||||
Db    421 GTCACAGACAATGAAAAAATGGTTGCAGACCTTGAAAACCCATTTATCTTAATTATGGAT 480

Qy    681 AAAAAAGTGTCAAACATCCAAGACATTTTGCCACTACTTGAGGAAGTTCTTAAAACCAAC 740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 AAAAAAGTGTCAAACATCCAAGACATTTTGCCACTACTTGAGGAAGTTCTTAAAACCAAC 540

Qy    741 CGTCCATTACTCATTATTGCAGATGATGTGGATGGTGAAGCACTTCCAACCCTTGTCTTG 800
          ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db    541 CGTCCATTACTCATTATTGCAGATGATGTGGATGGTGAAGCCCTTCCAACCCTTGTCTTG 600

Qy    801 AACAAGATTCGTGGTACTTTCAATGTGGTTGCTGTCAAAGCGCCAGGATTTGGTGATCGT 860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AACAAGATTCGTGGTACTTTCAATGTGGTTGCTGTCAAAGCGCCAGGATTTGGTGATCGT 660

Qy    861 CGTAAAGCTATGCTTGAAGACATTGCTATCTTGACAGGTGGTACAGTGATTACAGAGGAT 920
          |||||||||||||||||||||||||||||||||||||||| |||||||| ||||||||||||||
Db    661 CGTAAAGCTATGCTTGAAGACATTGCTATCTTGACTGGTGGTACTGTGATTACAGAGGAT 720

Qy    921 CTAGGACTTGAATTAAAAGATGCTACAATGACAGCCCTTGGACAGGCTGCTAAGATTACA 980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CTAGGACTTGAATTAAAAGATGCTACAATGACAGCCCTTGGACAGGCTGCTAAGATTACA 780

Qy    981 GTTGATAAAGATAGCACAGTAATTGTTGAAGGTTCAGGAAGTTCAGAAGCTATTGCTAAC 1040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GTTGATAAAGATAGCACAGTAATTGTTGAAGGTTCAGGAAGTTCAGAAGCTATTGCTAAC 840

Qy   1041 CGTATTGCACTGATTAAATCGCAATTAGAAACAACAACTTCTGACTTTGACCGTGAAAAA 1100
```

```
Db    841 CGCATTGCACTGATTAAATCGCAATTAGAAACAACAACTTCTGACTTTGACCGTGAAAAA 900

Qy   1101 CTACAAGAACGTTTGGCGAAATTAGCTGGTGGTGTAGCTGTTATCAAAGTAGGAGCTCCA 1160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 CTACAAGAACGTTTGGCGAAATTAGCTGGTGGTGTAGCTGTTATCAAAGTAGGAGCTCCA 960

Qy   1161 ACAGAGACAGCTTTAAAAGAAATGAAACTTCGCATTGAGGATGCTCTAAATGCTACACGT 1220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 ACAGAGACAGCTTTAAAAGAAATGAAACTTCGCATTGAGGATGCTCTAAATGCCACACGT 1020

Qy   1221 GCAGCCGTTGAAGAAGGTATCGTTGCTGGTGGTGGAACAGCACTTATTACGGTTATTGAA 1280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GCAGCCGTTGAAGAAGGTATCGTTGCTGGTGGTGGAACAGCACTTATTACGGTGATCGAA 1080

Qy   1281 AAAGTAGCAGCTCTTGAGCTTGAGGGCGATGATGCTACTGGACGTAACATTGTGCTTCGT 1340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 AAAGTAGCTGCTCTTGAGCTTGAGGGCGATGACGCTACTGGACGTAACATTGTGCTTCGT 1140

Qy   1341 GCTCTAGAAGAGCCTGTACGTCAAATTGCTTTAAATGCTGGGTACGAAGGCTCCGTAGTT 1400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GCTCTAGAAGAGCCTGTACGTCAAATTGCTTTAAATGCTGGGTACGAAGGCTCCGTAGTT 1200

Qy   1401 ATTGACAAGTTGAAAAACAGCCCTGCAGGAACAGGATTTAATGCTGCAACAGGTGAGTGG 1460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 ATTGACAAGTTGAAAAACAGCCCTGCAGGAACAGGATTTAATGCTGCAACAGGTGAGTGG 1260

Qy   1461 GTTGATATGATTAAAACAGGAATCATTGACCCTGTCAAAGTAACACGATCAGCGCTTCAA 1520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 GTTGATATGATTAAAACAGGAATCATTGACCCTGTCAAAGTAACACGATCAGCGCTTCAA 1320

Qy   1521 AATGCAGCTTCTGTAGCTAGTCTTATTTTGACAACAGAAGCAGTTGTTGCTAATAAACCT 1580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 AATGCAGCTTCTGTAGCTAGTCTTATTTTGACAACAGAAGCAGTTGTTGCTAATAAGCCT 1380

Qy   1581 GAACCAGCTACGCCAGCGCCAGCAATGCCAGCAGGTATGGATCCAGGAATGATGGGTGG 1639
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 GAACCAGCTGCGCCAGCGCCAGCAATGCCAGCAGGTATGGATCCAGGAATGATGGGCGG 1439
```

RESULT 6
AY121365

```
LOCUS       AY121365               1421 bp    DNA     linear   BCT 30-JUL-2002
DEFINITION  Streptococcus dysgalactiae subsp. equisimilis strain ATCC 12394
            chaperonin GroEL gene, partial cds.
ACCESSION   AY121365
VERSION     AY121365.1  GI:22022489
KEYWORDS    .
SOURCE      Streptococcus dysgalactiae subsp. equisimilis.
  ORGANISM  Streptococcus dysgalactiae subsp. equisimilis
            Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
            Streptococcus.
REFERENCE   1  (bases 1 to 1421)
  AUTHORS   Woo,P.C.Y., Teng,J.L.L., Lau,S.K.P., Lum,P.N.L., Leung,K.-W.,
            Tse,H., Wong,K.-L., Li,K.-W., Lam,K.-C. and Yuen,K.-Y.
  TITLE     Chaperonin GroEL gene of Group G Streptococcus dysgalactiae
            subspecies equisimilis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1421)
  AUTHORS   Woo,P.C.Y., Teng,J.L.L., Lau,S.K.P., Lum,P.N.L., Leung,K.-W.,
            Tse,H., Wong,K.-L., Li,K.-W., Lam,K.-C. and Yuen,K.-Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-JUN-2002) Microbiology, The University of Hong Kong,
            Pokfulam Road, Hong Kong, China
FEATURES             Location/Qualifiers
     source          1. .1421
                     /organism="Streptococcus dysgalactiae subsp. equisimilis"
                     /strain="ATCC 12394"
                     /sub_species="equisimilis"
                     /db_xref="ATCC:12394"
                     /db_xref="taxon:119602"
     CDS             <1. .>1421
                     /codon_start=3
                     /transl_table=11
                     /product="chaperonin GroEL"
                     /protein_id="AAM83128.1"
                     /db_xref="GI:22022490"
                     /translation="TVKVTLGPKGRNVVLEKAFGSPLITNDGVTIAKEIELEDHFENM
                     GAKLVSEVASKTNDIAGDGTTTATVLTQAIVREGLKNVTAGANPIGIRRGIETATATA
                     VEALKAIAQPVSGKEAIAQVAAVSSRSEKVGEYISEAMERVGNDGVITIEESRGMETE
                     LEVVEGMQFDRGYLSQYMVTDNEKMVADLENPFILITDKKVSNIQDILPLLEEVLKTN
                     RPLLIIADDVDGEALPTLVLNKIRGTFNVVAVKAPGFGDRRKAMLEDIAILTGGTVIT
                     EDLGLELKDATMPALGQAAKVTVDKDSTVIVEGAGSSEAIANRVGLIKSQLETTTSDF
                     DREKLQERLAKLAGGVAVIKVGAATETALKEMKLRIEDALNATRAAVEEGIVAGGGTA
                     LITVIEKVAALELDGDDATGRNIVLRALEEPVRQIAFNAGYEGSVVIDKLKNSPVGTG
                     FNAATGEWADMIAAGIIDPVKVT"
BASE COUNT      417 a    273 c    354 g    377 t
ORIGIN
```

```
  Query Match           70.5%;  Score 1170.4;  DB 1;  Length 1421;
  Best Local Similarity  89.0%;  Pred. No. 1e-228;
  Matches 1264;  Conservative    0;  Mismatches  156;  Indels    0;  Gaps    0;

Qy     85 ATACCGTCAAAGTAACGCTTGGTCCTAAAGGGCGCAATGTTGTTCTTGAAAAAGCTTTTG 144
          | || || ||||||||||||||||||||||| || || || ||||||||||||||||||||
Db      1 ACACGGTAAAAGTAACGCTTGGTCCTAAAGGTCGTAACGTGGTTCTTGAAAAAGCTTTTG 60

Qy    145 GTTCTCCCTTAATTACTAATGACGGGGTAACCATTGCTAAAGAGATCGAATTAGAAGATC 204
          | ||||| || ||||| |||||||||||| |||||||||||||||| |||||||||||
Db     61 GATCTCCTTTGATTACCAATGACGGGGTTACCATTGCTAAAGAGATTGAATTAGAAGACC 120

Qy    205 ATTTTGAAAACATGGGAGCAAAATTGGTGTCTGAAGTGGCTTCTAAAACCAATGATATTG 264
          ||||||| || |||||||| |||||||| |||||||| |||||||||||||||||||| |
Db    121 ATTTTGAGAATATGGGAGCTAAATTGGTTTCTGAAGTTGCTTCTAAAACCAATGATATCG 180

Qy    265 CTGGTGATGGGACGACTACTGCAACAGTTTTGACACAAGCCATTGTTCATGAAGGACTAA 324
          | ||||| || || || |||||||||| |||||||| || || || | |||||| || |
Db    181 CAGGTGACGGAACCACAACTGCAACAGTATTGACACAGGCTATCGTCCGTGAAGGGCTTA 240

Qy    325 AAAATGTGACAGCAGGTGCTAATCCAATTGGTATCCGTCGAGGCATTGAAACAGCAACAG 384
          ||||||| || || ||||| || |||||||||| ||||| || ||||||||||||||||||
Db    241 AAAATGTAACTGCTGGTGCCAACCCAATTGGTATTCGTCGTGGGATTGAAACAGCAACAG 300

Qy    385 CAACAGCTGTTGAAGCCTTGAAAGCCATTGCTCAACCTGTATCTGGCAAGGAAGCTATTG 444
          ||||||| |||||||||||||||| |||||||| ||||| ||||| || ||||| ||||
Db    301 CAACAGCCGTTGAAGCCTTGAAAGCTATTGCTCAGCCTGTTTCTGGTAAAGAAGCGATTG 360

Qy    445 CTCAGGTCGCTGCAGTATCATCACGCTCTGAAAAAGTTGGAGAGTATATCTCAGAAGCTA 504
          |||| || ||||| || ||||| || |||||||||||||||||| || |||||||||| |
Db    361 CTCAAGTTGCTGCTGTGTCATCTCGTTCTGAAAAAGTTGGAGAATACATCTCAGAAGCCA 420

Qy    505 TGGAGCGTGTGGGCAACGATGGTGTGATTACCATCGAAGAATCTCGAGGTATGGAAACAG 564
          |||| |||||||||||| || |||||| |||||||||||||||||| || |||||||| ||||
Db    421 TGGAACGTGTGGGCAATGACGGTGTCATTACCATCGAAGAATCACGTGGTATGGAGACAG 480

Qy    565 AACTTGAAGTGGTTGAAGGCATGCAATTTGACCGTGGTTACCTGTCTCAATACATGGTCA 624
          | |||||||||||| |||||||||| ||||| |||||||||||||||||||||||||||||
Db    481 AGCTTGAAGTGGTAGAAGGCATGCAGTTTGATCGTGGTTACCTGTCTCAATACATGGTCA 540

Qy    625 CAGACAATGAAAAAAATGGTTGCAGACCTTGAAAACCCATTTATCTTAATCACGGATAAAA 684
          |||||||||||||||||||||||||||||||||||||||||||||| || ||||||||||
Db    541 CAGACAATGAAAAAATGGTTGCAGACCTTGAAAACCCATTTATCTTGATTACGGATAAAA 600

Qy    685 AAGTGTCAAACATCCAAGACATTTTGCCACTACTTGAGGAAGTTCTTAAAACCAACCGTC 744
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AAGTGTCAAACATCCAAGACATTTTGCCACTACTTGAGGAAGTTCTTAAAACCAACCGTC 660

Qy    745 CATTACTCATTATTGCAGATGATGTGGATGGTGAAGCACTTCCAACCCTTGTCTTGAACA 804
          |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db    661 CATTACTCATTATTGCAGATGATGTGGATGGTGAAGCCCTTCCAACCCTTGTCTTGAACA 720

Qy    805 AGATTCGTGGTACTTTCAATGTGGTTGCTGTCAAAGCGCCAGGATTTGGTGATCGTCGTA 864
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db    721 AGATTCGTGGTACTTTCAATGTGGTTGCTGTCAAAGCGCCAGGATTTGGTGATCGCCGTA 780

Qy    865 AAGCTATGCTTGAAGACATTGCTATCTTGACAGGTGGTACAGTGATTACAGAGGATCTAG 924
```

```
Db    781 AAGCTATGCTTGAAGACATTGCTATCTTGACAGGTGGTACAGTGATTACAGAGGATCTAG 840

Qy    925 GACTTGAATTAAAAGATGCTACAATGACAGCCCTTGGACAGGCTGCTAAGATTACAGTTG 984

Db    841 GACTTGAATTAAAAGATGCTACAATGCCAGCTCTTGGTCAAGCTGCTAAAGTGACTGTGG 900

Qy    985 ATAAAGATAGCACAGTAATTGTTGAAGGTTCAGGAAGTTCAGAAGCTATTGCTAACCGTA 1044

Db    901 ATAAAGACAGCACAGTTATTGTGGAAGGTGCAGGAAGTTCTGAAGCCATTGCCAACCGTG 960

Qy   1045 TTGCACTGATTAAATCGCAATTAGAAACAACAACTTCTGACTTTGACCGTGAAAAACTAC 1104

Db    961 TTGGCTTGATTAAGTCACAACTAGAAACCACAACGTCTGACTTTGACCGTGAAAAATTAC 1020

Qy   1105 AAGAACGTTTGGCGAAATTAGCTGGTGGTGTAGCTGTTATCAAAGTAGGAGCTCCAACAG 1164

Db   1021 AAGAACGCTTGGCGAAATTAGCTGGTGGTGTGGCTGTCATCAAGGTAGGTGCTGCAACAG 1080

Qy   1165 AGACAGCTTTAAAAGAAATGAAACTTCGCATTGAGGATGCTCTAAATGCTACACGTGCAG 1224

Db   1081 AAACAGCCCTTAAAGAAATGAAACTTCGTATCGAAGATGCCTTGAATGCCACACGTGCAG 1140

Qy   1225 CCGTTGAAGAAGGTATCGTTGCTGGTGGTGGAACAGCACTTATTACGGTTATTGAAAAAG 1284

Db   1141 CCGTTGAAGAAGGTATCGTTGCTGGTGGTGGAACAGCACTTATTACGGTGATCGAAAAAG 1200

Qy   1285 TAGCAGCTCTTGAGCTTGAGGGCGATGATGCTACTGGACGTAACATTGTGCTTCGTGCTC 1344

Db   1201 TAGCTGCTCTTGAGCTTGATGGCGATGACGCTACTGGCCGCAATATCGTTCTTCGTGCGT 1260

Qy   1345 TAGAAGAGCCTGTACGTCAAATTGCTTTAAATGCTGGGTACGAAGGCTCCGTAGTTATTG 1404

Db   1261 TGGAAGAACCTGTTCGTCAAATTGCATTCAACGCTGGTTACGAAGGTTCCGTTGTCATCG 1320

Qy   1405 ACAAGTTGAAAAACAGCCCTGCAGGAACAGGATTTAATGCTGCAACAGGTGAGTGGGTTG 1464

Db   1321 ACAAATTGAAAAATAGCCCTGTTGGAACAGGCTTTAATGCGGCAACAGGTGAATGGGCAG 1380

Qy   1465 ATATGATTAAAACAGGAATCATTGACCCTGTCAAAGTAAC 1504

Db   1381 ATATGATTGCGGCAGGTATTATCGATCCTGTTAAAGTAAC 1420


RESULT 7
AX148806
LOCUS       AX148806                1306 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 8 from Patent WO0136625.
ACCESSION   AX148806
VERSION     AX148806.1  GI:14347330
KEYWORDS    .
SOURCE      Streptococcus pyogenes.
  ORGANISM  Streptococcus pyogenes
            Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
            Streptococcus.
REFERENCE   1  (bases 1 to 1306)
  AUTHORS   Wright,J.A., Young,A.H. and Dugourd,D.
  TITLE     Antisense oligonucleotide sequences derived from groel and groes as
            inhibitors of microorganisms
  JOURNAL   Patent: WO 0136625-A 8 25-MAY-2001;
            GeneSense Technologies Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .1306
                     /organism="Streptococcus pyogenes"
                     /db_xref="taxon:1314"
BASE COUNT      407 a    235 c    308 g    356 t
ORIGIN

  Query Match           68.7%;  Score 1140.4;  DB 6;  Length 1306;
  Best Local Similarity   99.9%;  Pred. No. 1.4e-222;
  Matches 1141;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    498 GAAGCTATGGAGCGTGTGGGCAACGATGGTGTGATTACCATCGAAGAATCTCGAGGTATG 557

Db      2 GAAGCTATGGAGCGTGTGGGCAACGATGGTGTGATTACCATCGAAGAATCTCGAGGTATG 61

Qy    558 GAAACAGAACTTGAAGTGGTTGAAGGCATGCAATTTGACCGTGGTTACCTGTCTCAATAC 617

Db     62 GAAACAGAACTTGAAGTGGTTGAAGGCATGCAATTTGACCGTGGTTACCTGTCTCAATAC 121

Qy    618 ATGGTCACAGACAATGAAAAAATGGTTGCAGACCTTGAAAACCCATTTATCTTAATCACG 677

Db    122 ATGGTCACAGACAATGAAAAAATGGTTGCAGACCTTGAAAACCCATTTATCTTAATCACG 181

Qy    678 GATAAAAAAGTGTCAAACATCCAAGACATTTTGCCACTACTTGAGGAAGTTCTTAAAACC 737

Db    182 GATAAAAAAGTGTCAAACATCCAAGACATTTTGCCACTACTTGAGGAAGTTCTTAAAACC 241

Qy    738 AACCGTCCATTACTCATTATTGCAGATGATGTGGATGGTGAAGCACTTCCAACCCTTGTC 797

Db    242 AACCGTCCATTACTCATTATTGCAGATGATGTGGATGGTGAAGCACTTCCAACCCTTGTC 301

Qy    798 TTGAACAAGATTCGTGGTACTTTCAATGTGGTTGCTGTCAAAGCGCCAGGATTTGGTGAT 857

Db    302 TTGAACAAGATTCGTGGTACTTTCAATGTGGTTGCTGTCAAAGCGCCAGGATTTGGTGAT 361

Qy    858 CGTCGTAAAGCTATGCTTGAAGACATTGCTATCTTGACAGGTGGTACAGTGATTACAGAG 917

Db    362 CGTCGTAAAGCTATGCTTGAAGACATTGCTATCTTGACAGGTGGTACAGTGATTACAGAG 421

Qy    918 GATCTAGGACTTGAATTAAAAGATGCTACAATGACAGCCCTTGGACAGGCTGCTAAGATT 977

Db    422 GATCTAGGACTTGAATTAAAAGATGCTACAATGACAGCCCTTGGACAGGCTGCTAAGATT 481

Qy    978 ACAGTTGATAAAGATAGCACAGTAATTGTTGAAGGTTCAGGAAGTTCAGAAGCTATTGCT 1037

Db    482 ACAGTTGATAAAGATAGCACAGTAATTGTTGAAGGTTCAGGAAGTTCAGAAGCTATTGCT 541

Qy   1038 AACCGTATTGCACTGATTAAATCGCAATTAGAAACAACAACTTCTGACTTTGACCGTGAA 1097

Db    542 AACCGTATTGCACTGATTAAATCGCAATTAGAAACAACAACTTCTGACTTTGACCGTGAA 601

Qy   1098 AAACTACAAGAACGTTTGGCGAAATTAGCTGGTGGTGTAGCTGTTATCAAAGTAGGAGCT 1157

Db    602 AAACTACAAGAACGTTTGGCGAAATTAGCTGGTGGTGTAGCTGTTATCAAAGTAGGAGCT 661

Qy   1158 CCAACAGAGACAGCTTTAAAAGAAATGAAACTTCGCATTGAGGATGCTCTAAATGCTACA 1217

Db    662 CCAACAGAGACAGCTTTAAAAGAAATGAAACTTCGCATTGAGGATGCTCTAAATGCTACA 721

Qy   1218 CGTGCAGCCGTTGAAGAAGGTATCGTTGCTGGTGGTGGAACAGCACTTATTACGGTTATT 1277

Db    722 CGTGCAGCCGTTGAAGAAGGTATCGTTGCTGGTGGTGGAACAGCACTTATTACGGTTATT 781

Qy   1278 GAAAAAGTAGCAGCTCTTGAGCTTGAGGGCGATGATGCTACTGGACGTAACATTGTGCTT 1337

Db    782 GAAAAAGTAGCAGCTCTTGAGCTTGAGGGCGATGATGCTACTGGACGTAACATTGTGCTT 841

Qy   1338 CGTGCTCTAGAAGAGCCTGTACGTCAAATTGCTTTAAATGCTGGGTACGAAGGCTCCGTA 1397

Db    842 CGTGCTCTAGAAGAGCCTGTACGTCAAATTGCTTTAAATGCTGGGTACGAAGGCTCCGTA 901

Qy   1398 GTTATTGACAAGTTGAAAAACAGCCCTGCAGGAACAGGATTTAATGCTGCAACAGGTGAG 1457

Db    902 GTTATTGACAAGTTGAAAAACAGCCCTGCAGGAACAGGATTTAATGCTGCAACAGGTGAG 961

Qy   1458 TGGGTTGATATGATTAAAACAGGAATCATTGACCCTGTCAAAGTAACACGATCAGCGCTT 1517

Db    962 TGGGTTGATATGATTAAAACAGGAATCATTGACCCTGTCAAAGTAACACGATCAGCGCTT 1021

Qy   1518 CAAAATGCAGCTTCTGTAGCTAGTCTTATTTTGACAACAGAAGCAGTTGTTGCTAATAAA 1577

Db   1022 CAAAATGCAGCTTCTGTAGCTAGTCTTATTTTGACAACAGAAGCAGTTGTTGCTAATAAA 1081

Qy   1578 CCTGAACCAGCTACGCCAGCGCCAGCAATGCCAGCAGGTATGGATCCAGGAATGATGGGT 1637
```

```
Db    1082 CCTGAACCAGCTACGCCAGCGCCAGCAATGCCAGCAGGTATGGATCCAGGAATGATGGGC 1141

Qy    1638 GG 1639
           ||
Db    1142 GG 1143


RESULT 8
AY121364
LOCUS       AY121364                1421 bp    DNA     linear   BCT 30-JUL-2002
DEFINITION  Streptococcus dysgalactiae subsp. equisimilis strain ATCC 35666
            chaperonin GroEL gene, partial cds.
ACCESSION   AY121364
VERSION     AY121364.1  GI:22022487
KEYWORDS    .
SOURCE      Streptococcus dysgalactiae subsp. equisimilis.
  ORGANISM  Streptococcus dysgalactiae subsp. equisimilis
            Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
            Streptococcus.
REFERENCE   1  (bases 1 to 1421)
  AUTHORS   Woo,P.C.Y., Teng,J.L.L., Lau,S.K.P., Lum,P.N.L., Leung,K.-W.,
            Tse,H., Wong,K.-L., Li,K.-W., Lam,K.-C. and Yuen,K.-Y.
  TITLE     Chaperonin GroEL gene of Group C Streptococcus dysgalactiae
            subspecies equisimilis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1421)
  AUTHORS   Woo,P.C.Y., Teng,J.L.L., Lau,S.K.P., Lum,P.N.L., Leung,K.-W.,
            Tse,H., Wong,K.-L., Li,K.-W., Lam,K.-C. and Yuen,K.-Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-JUN-2002) Microbiology, The University of Hong Kong,
            Pokfulam Road, Hong Kong, China
FEATURES             Location/Qualifiers
     source          1. .1421
                     /organism="Streptococcus dysgalactiae subsp. equisimilis"
                     /strain="ATCC 35666"
                     /sub_species="equisimilis"
                     /db_xref="ATCC:35666"
                     /db_xref="taxon:119602"
     CDS             <1. .>1421
                     /codon_start=3
                     /transl_table=11
                     /product="chaperonin GroEL"
                     /protein_id="AAM83127.1"
                     /db_xref="GI:22022488"
                     /translation="VTLGPKGRNVVLEKAFGSPLITNDGVTIAKEIELEDHFENMGAK
                     LVSEVASKTNDIAGDGTTTATVLTQAIVREGLKNVTAGANPIGIRRGIETATATAVEA
                     LKAIAQPVSGKEAIAQVAAVSSRSEKVGEYISEAMERVGNDGVITIEESRGMETELEV
                     VEGMQFDRGYLSQYMVTDNEKMVADLENPFILITDKKVSNIQDILPLLEEVLKTNRPL
                     LIIADDVDGEALPTLVLNKIRGTFNVVAVKAPGFGDRRKAMLEDIAILTGGTVITEDL
                     GLELKDATMPALGQAAKVTVDKDSTVIVEGAGSSEAIANRVGLIKSQLETTTSDFDRE
                     KLQERLAKLAGGVAVIKVGAATETALKEMKLRIEDALNATRAAVEEGIVAGGGTALIT
                     VIEKVAALELDGDDATGRNIVLRALEEPVRQIAFNAGYEGSVVIDKLKNSPVGTGFNA
                     ATGEWVDMIAAGIIDPVKVTRSA"
BASE COUNT      408 a    275 c    354 g    384 t
ORIGIN

  Query Match             68.0%;  Score 1128.8;  DB 1;  Length 1421;
  Best Local Similarity   87.2%;  Pred. No. 3.2e-220;
  Matches 1238;  Conservative    0;  Mismatches  182;  Indels    0;  Gaps    0;

Qy      94 AAGTAACGCTTGGTCCTAAAGGGCGCAATGTTGTTCTTGAAAAAGCTTTTGGTTCTCCCT 153
           ||||||||||||||||||||| || || || ||||||||||||||||||||| ||||| |
Db       1 AAGTAACGCTTGGTCCTAAAGGTCGTAACGTGGTTCTTGAAAAAGCTTTTGGATCTCCTT 60

Qy     154 TAATTACTAATGACGGGGTAACCATTGCTAAAGAGATCGAATTAGAAGATCATTTTGAAA 213
           | ||||| |||||||||||| |||||||||||||||||| |||||||||| |||||||| |
Db      61 TGATTACCAATGACGGGGTTACCATTGCTAAAGAGATTGAATTAGAAGACCATTTTGAGA 120

Qy     214 ACATGGGAGCAAAATTGGTGTCTGAAGTGGCTTCTAAAACCAATGATATTGCTGGTGATG 273
           | |||||||| |||||||| |||||||||||||||||||| || ||||| |
Db     121 ATATGGGAGCTAAATTGGTTTCTGAAGTTGCTTCTAAAACCAATGATATCGCAGGTGACG 180

Qy     274 GGACGACTACTGCAACAGTTTTGACACAAGCCATTGTTCATGAAGGACTAAAAAATGTGA 333
           | || || |||||||||| |||||||| || || || | |||||| || |||||||| |
Db     181 GAACCACAACTGCAACAGTATTGACACAGGCTATCGTCCGTGAAGGGCTTAAAAATGTAA 240

Qy     334 CAGCAGGTGCTAATCCAATTGGTATCCGTCGAGGCATTGAAACAGCAACAGCAACAGCTG 393
           |.|| ||||| || |||||||||| ||||| || ||||||||||||||||||||||| |
Db     241 CTGCTGGTGCCAACCCAATTGGTATTCGTCGTGGGATTGAAACAGCAACAGCAACAGCCG 300

Qy     394 TTGAAGCCTTGAAAGCCATTGCTCAACCTGTATCTGGCAAGGAAGCTATTGCTCAGGTCG 453
           |||||||||||||||| |||||||| ||||| ||||| || ||||| |||||||| || |
Db     301 TTGAAGCCTTGAAAGCTATTGCTCAGCCTGTTTCTGGTAAAGAAGCGATTGCTCAAGTTG 360

Qy     454 CTGCAGTATCATCACGCTCTGAAAAAGTTGGAGAGTATATCTCAGAAGCTATGGAGCGTG 513
           |||| || ||||| || |||||||||||||||| || |||||||||| ||||| ||||
Db     361 CTGCTGTGTCATCTCGTTCTGAAAAAGTTGGAGAATACATCTCAGAAGCCATGGAACGTG 420

Qy     514 TGGGCAACGATGGTGTGATTACCATCGAAGAATCTCGAGGTATGGAAACAGAACTTGAAG 573
           ||||||| || ||||| |||||||||||||||| || |||||||| ||||| |||||||
Db     421 TGGGCAATGACGGTGTCATTACCATCGAAGAATCACGTGGTATGGAGACAGAGCTTGAAG 480

Qy     574 TGGTTGAAGGCATGCAATTTGACCGTGGTTACCTGTCTCAATACATGGTCACAGACAATG 633
           |||| |||||||||| ||||| |||||||||||||||||||||||||||||||||||||
Db     481 TGGTAGAAGGCATGCAGTTTGATCGTGGTTACCTGTCTCAATACATGGTCACAGACAATG 540

Qy     634 AAAAAATGGTTGCAGACCTTGAAAACCCATTTATCTTAATCACGGATAAAAAAGTGTCAA 693
           |||||||||||||||||||| |||||||||||||| || || || ||||||||||||||
Db     541 AAAAAATGGTTGCAGACCTTGAGAACCCATTTATCTTGATTACTGACAAAAAAGTGTCAA 600

Qy     694 ACATCCAAGACATTTTGCCACTACTTGAGGAAGTTCTTAAAACCAACCGTCCATTACTCA 753
           |||||||||| ||| | ||| | ||||||||||||||||||||||||||||||| | |
Db     601 ACATCCAAGATATTCTCCCATTGCTTGAGGAAGTTCTTAAAACCAACCGTCCATTGTTGA 660

Qy     754 TTATTGCAGATGATGTGGATGGTGAAGCACTTCCAACCCTTGTCTTGAACAAGATTCGTG 813
           |||| || ||||| || ||||| ||||| |||||||||||||| ||||| || |||||||
Db     661 TTATCGCCGATGACGTTGATGGCGAAGCTCTTCCAACCCTTGTTTTGAATAAAATTCGTG 720

Qy     814 GTACTTTCAATGTGGTTGCTGTCAAAGCGCCAGGATTTGGTGATCGTCGTAAAGCTATGC 873
           |||||||||||||||||||||||||||||| |||||||||||||||| ||||||||||||
Db     721 GTACTTTCAATGTGGTTGCTGTCAAAGCTCCAGGATTTGGTGATCGCCGTAAAGCTATGC 780

Qy     874 TTGAAGACATTGCTATCTTGACAGGTGGTACAGTGATTACAGAGGATCTAGGACTTGAAT 933
           |||| ||||| |||||||||||||||||||||||||||||| |||||||| ||  | || |||||||
Db     781 TTGAGGACATCGCTATCTTGACAGGTGGTACAGTCATTACAGAAGACTTGGGTCTTGAAT 840

Qy     934 TAAAAGATGCTACAATGACAGCCCTTGGACAGGCTGCTAAGATTACAGTTGATAAAGATA 993
           | ||||| ||||| ||| |||| ||||| || |||||||| | || || |||||||| |
Db     841 TGAAAGACGCTACGATGCCAGCTCTTGGTCAAGCTGCTAAAGTGACTGTGGATAAAGACA 900

Qy     994 GCACAGTAATTGTTGAAGGTTCAGGAAGTTCAGAAGCTATTGCTAACCGTATTGCACTGA 1053
           ||||||| |||| |||||| |||||||||| ||||| ||||| |||||| |||   |||
Db     901 GCACAGTTATTGTGGAAGGTGCAGGAAGTTCTGAAGCCATTGCCAACCGTGTTGGCTTGA 960

Qy    1054 TTAAATCGCAATTAGAAACAACAACTTCTGACTTTGACCGTGAAAAACTACAAGAACGTT 1113
           |||| || ||| ||||||| ||||| |||||||||||||||||||||| ||||||||| |
Db     961 TTAAGTCACAACTAGAAACCACAACGTCTGACTTTGACCGTGAAAAATTACAAGAACGCT 1020

Qy    1114 TGGCGAAATTAGCTGGTGGTGTAGCTGTTATCAAAGTAGGAGCTCCAACAGAGACAGCTT 1173
           |||||||||||||||||||| ||||| ||||| ||||| ||| ||||||| |||||
Db    1021 TGGCGAAATTAGCTGGTGGTGTGGCTGTCATCAAGGTAGGTGCTGCAACAGAAACAGCCC 1080

Qy    1174 TAAAAGAAATGAAACTTCGCATTGAGGATGCTCTAAATGCTACACGTGCAGCCGTTGAAG 1233
           | |||||||||||||||| || || |||||  | ||||| ||||||||||||||||||||
Db    1081 TTAAAGAAATGAAACTTCGTATCGAAGATGCCTTGAATGCCACACGTGCAGCCGTTGAAG 1140

Qy    1234 AAGGTATCGTTGCTGGTGGTGGAACAGCACTTATTACGGTTATTGAAAAAGTAGCAGCTC 1293
           |||||||||||||||||||||||||||||||||||||||||| || |||||||||| ||||
Db    1141 AAGGTATCGTTGCTGGTGGTGGAACAGCACTTATTACGGTGATCGAAAAAGTAGCTGCTC 1200

Qy    1294 TTGAGCTTGAGGGCGATGATGCTACTGGACGTAACATTGTGCTTCGTGCTCTAGAAGAGC 1353
           |||||||||| |||||||| |||||||| ||||| || || |||||||  |||||| |
Db    1201 TTGAGCTTGATGGCGATGACGCTACTGGCCGTAATATCGTTCTTCGTGCGTTAGAAGAAC 1260

Qy    1354 CTGTACGTCAAATTGCTTTAAATGCTGGGTACGAAGGCTCCGTAGTTATTGACAAGTTGA 1413
           |||| |||||||||||| || || |||||| |||||||| ||||| ||||| ||||| ||||
```

```
Db   1261 CTGTTCGTCAAATTGCATTCAACGCTGGTTACGAAGGTTCCGTTGTTATCGACAAATTGA 1320

Qy   1414 AAAACAGCCCTGCAGGAACAGGATTTAATGCTGCAACAGGTGAGTGGGTTGATATGATTA 1473
          |||| |||||||  ||||||||| |||||||| |||||||||| ||||| |||||||||
Db   1321 AAAATAGCCCTGTTGGAACAGGCTTTAATGCGGCAACAGGTGAATGGGTAGATATGATTG 1380

Qy   1474 AAACAGGAATCATTGACCCTGTCAAAGTAACACGATCAGC 1513
          |||| || || || ||||| |||||||| || |||||
Db   1381 CGGCAGGTATTATCGATCCTGTTAAAGTAACCCGTTCAGC 1420


RESULT 9
AY121366
LOCUS       AY121366               1422 bp    DNA     linear   BCT 30-JUL-2002
DEFINITION  Streptococcus dysgalactiae subsp. equisimilis strain CIP 55-123
            chaperonin GroEL gene, partial cds.
ACCESSION   AY121366
VERSION     AY121366.1  GI:22022491
KEYWORDS    .
SOURCE      Streptococcus dysgalactiae subsp. equisimilis.
  ORGANISM  Streptococcus dysgalactiae subsp. equisimilis
            Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
            Streptococcus.
REFERENCE   1  (bases 1 to 1422)
  AUTHORS   Woo,P.C.Y., Teng,J.L.L., Lau,S.K.P., Lum,P.N.L., Leung,K.-W.,
            Tse,H., Wong,K.-L., Li,K.-W., Lam,K.-C. and Yuen,K.-Y.
  TITLE     Chaperonin GroEL gene of Group L Streptococcus dysgalactiae
            subspecies equisimilis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1422)
  AUTHORS   Woo,P.C.Y., Teng,J.L.L., Lau,S.K.P., Lum,P.N.L., Leung,K.-W.,
            Tse,H., Wong,K.-L., Li,K.-W., Lam,K.-C. and Yuen,K.-Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-JUN-2002) Microbiology, The University of Hong Kong,
            Pokfulam Road, Hong Kong, China
FEATURES             Location/Qualifiers
     source          1. .1422
                     /organism="Streptococcus dysgalactiae subsp. equisimilis"
                     /strain="CIP 55-123"
                     /sub_species="equisimilis"
                     /db_xref="taxon:119602"
     CDS             <1. .>1422
                     /codon_start=1
                     /transl_table=11
                     /product="chaperonin GroEL"
                     /protein_id="AAM83129.1"
                     /db_xref="GI:22022492"
                     /translation="KVTLGPKGRNVVLEKAFGSPLITNDGVTIAKEIELEDHFENMGA
                     KLVSEVASKTNDIAGDGTTTATVLTQAIVREGLKNVTAGANPIGIRRGIETATATAVE
                     ALKAIAQPVSGKEAIAQVAAVSSRSEKVGEYISEAMERVGNDGVITIEESRGMETELE
                     VVEGMQFDRGYLSQYMVTDNEKMVADLENPFILITDKKVSNIQDILPLLEEVLKTNRP
                     LLIIADDVDGEALPTLVLNKIRGTFNVVAVKAPGFGDRRKAMLEDIAILTGGTVITED
                     LGLELKDATMPALGQAAKVTVDKDSTVIVEGAGSSEAIANRVGLIKSQLETTTSDFDR
                     EKLHERLAKLAGGVAVIKVGAATETALKEMKLRIEDALNATRAAVEEGIVAGGGTALI
                     TVIEKVAALELDGDDATGRNIVLRALEEPVRQIAFNAGYEGSVVIDKLKNSPVGTGFN
                     AATGEWVDMIAAGIIDPVKVTRSA"
BASE COUNT      407 a    278 c    354 g    383 t
ORIGIN

  Query Match           67.7%;  Score 1125;  DB 1;  Length 1422;
  Best Local Similarity  87.0%;  Pred. No. 1.9e-219;
  Matches 1236;  Conservative    0;  Mismatches  185;  Indels    0;  Gaps    0;

Qy      93 AAAGTAACGCTTGGTCCTAAAGGGCGCAATGTTGTTCTTGAAAAAGCTTTTGGTTCTCCC 152
           ||||||||||||||||||||||| || || || ||||||||||||||||||| |||||
Db       1 AAAGTAACGCTTGGTCCTAAAGGTCGTAACGTGGTTCTTGAAAAAGCTTTTGGATCTCCT 60

Qy     153 TTAATTACTAATGACGGGGTAACCATTGCTAAAGAGATCGAATTAGAAGATCATTTTGAA 212
           || ||||| |||||||||| |||||||||||||||| |||||||||| ||||||||
Db      61 TTGATTACCAATGACGGGGTTACCATTGCTAAAGAGATTGAATTAGAAGACCATTTTGAG 120

Qy     213 AACATGGGAGCAAAATTGGTGTCTGAAGTGGCTTCTAAAACCAATGATATTGCTGGTGAT 272
           || |||||||| |||||||| |||||||| |||||||||||||||||||| || |||||

Db     121 AATATGGGAGCTAAATTGGTTTCTGAAGTTGCTTCTAAAACCAATGATATCGCAGGTGAC 180

Qy     273 GGGACGACTACTGCAACAGTTTTGACACAAGCCATTGTTCATGAAGGACTAAAAAATGTG 332
           || || || |||||||||| |||||||| || || || | |||||| || ||||||||
Db     181 GGAACCACAACTGCAACAGTATTGACACAGGCTATCGTCCGTGAAGGGCTTAAAAATGTA 240

Qy     333 ACAGCAGGTGCTAATCCAATTGGTATCCGTCGAGGCATTGAAACAGCAACAGCAACAGCT 392
           || || ||||| || |||||||||| |||||| || ||||||||||||||||||||||||
Db     241 ACTGCTGGTGCCAACCCAATTGGTATTCGTCGTGGGATTGAAACAGCAACAGCAACAGCC 300

Qy     393 GTTGAAGCCTTGAAAGCCATTGCTCAACCTGTATCTGGCAAGGAAGCTATTGCTCAGGTC 452
           |||||||||||||||| |||||||| |||||| |||||| || ||||| |||||||| ||
Db     301 GTTGAAGCCTTGAAAGCTATTGCTCAGCCTGTTTCTGGTAAAGAAGCGATTGCTCAAGTT 360

Qy     453 GCTGCAGTATCATCACGCTCTGAAAAAGTTGGAGAGTATATCTCAGAAGCTATGGAGCGT 512
           ||||| || ||||| || |||||||||||||||| || |||||||||| ||||| |||
Db     361 GCTGCTGTGTCATCTCGTTCTGAAAAAGTTGGAGAATACATCTCAGAAGCCATGGAACGT 420

Qy     513 GTGGGCAACGATGGTGTGATTACCATCGAAGAATCTCGAGGTATGGAAACAGAACTTGAA 572
           |||||||| || |||||| |||||||||||||||| || |||||||| ||||| ||||||
Db     421 GTGGGCAATGACGGTGTCATTACCATCGAAGAATCACGTGGTATGGAGACAGAGCTTGAA 480

Qy     573 GTGGTTGAAGGCATGCAATTTGACCGTGGTTACCTGTCTCAATACATGGTCACAGACAAT 632
           ||||| |||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db     481 GTGGTAGAAGGCATGCAGTTTGACCGTGGTTACCTGTCTCAATACATGGTCACAGACAAT 540

Qy     633 GAAAAAATGGTTGCAGACCTTGAAAACCCATTTATCTTAATCACGGATAAAAAAGTGTCA 692
           |||||||||||||||||||||| |||||||||||||| || || || ||||||||||||
Db     541 GAAAAAATGGTTGCAGACCTTGAGAACCCATTTATCTTGATTACTGACAAAAAAGTGTCA 600

Qy     693 AACATCCAAGACATTTTGCCACTACTTGAGGAAGTTCTTAAAACCAACCGTCCATTACTC 752
           |||||||||| ||| | ||| ||||||||||||||||||||||||||||||||| | |
Db     601 AACATCCAAGATATTCTCCCATTACTTGAGGAAGTTCTTAAAACCAACCGTCCATTGTTG 660

Qy     753 ATTATTGCAGATGATGTGGATGGTGAAGCACTTCCAACCCTTGTCTTGAACAAGATTCGT 812
           ||||| || ||||| || ||||| |||||||||||||||||||||||| |||| || ||||||
Db     661 ATTATCGCCGATGACGTTGATGGCGAAGCTCTTCCAACCCTTGTTTTGAATAAAATTCGT 720

Qy     813 GGTACTTTCAATGTGGTTGCTGTCAAAGCGCCAGGATTTGGTGATCGTCGTAAAGCTATG 872
           |||||||||||||||||||||||||||||| |||||||||||||||| ||||||||||||
Db     721 GGTACTTTCAATGTGGTTGCTGTCAAAGCTCCAGGATTTGGTGATCGCCGTAAAGCTATG 780

Qy     873 CTTGAAGACATTGCTATCTTGACAGGTGGTACAGTGATTACAGAGGATCTAGGACTTGAA 932
           ||||| |||| |||||||||||||||||||||||||| |||||||| ||  | || ||||||
Db     781 CTTGAGGACATCGCTATCTTGACAGGTGGTACAGTCATTACAGAAGACTTGGGTCTTGAA 840

Qy     933 TTAAAAGATGCTACAATGACAGCCCTTGGACAGGCTGCTAAGATTACAGTTGATAAAGAT 992
           || ||||| ||||||||| |||| ||||| || || ||||| | || || ||||||||
Db     841 TTGAAAGACGCTACAATGCCAGCTCTTGGTCAAGCCGCTAAAGTGACTGTGGATAAAGAC 900

Qy     993 AGCACAGTAATTGTTGAAGGTTCAGGAAGTTCAGAAGCTATTGCTAACCGTATTGCACTG 1052
           |||||||| |||| |||||| |||||||||| ||||| ||||| |||||| |||   ||
Db     901 AGCACAGTTATTGTGGAAGGTGCAGGAAGTTCTGAAGCCATTGCCAACCGTGTTGGCTTG 960

Qy    1053 ATTAAATCGCAATTAGAAACAACAACTTCTGACTTTGACCGTGAAAAACTACAAGAACGT 1112
           ||||| || ||| |||||||| ||||| |||||||||||||||||||||| |||| |||||
Db     961 ATTAAGTCACAACTAGAAACCACAACGTCTGACTTTGACCGTGAAAAATTACATGAACGC 1020

Qy    1113 TTGGCGAAATTAGCTGGTGGTGTAGCTGTTATCAAAGTAGGAGCTCCAACAGAGACAGCT 1172
           |||||||||||||||||||||| ||||| ||||| ||||| ||| ||||||| || ||
Db    1021 TTGGCGAAATTAGCTGGTGGTGTGGCTGTCATCAAGGTAGGTGCTGCAACAGAAACTGCC 1080

Qy    1173 TTAAAAGAAATGAAACTTCGCATTGAGGATGCTCTAAATGCTACACGTGCAGCCGTTGAA 1232
           | |||||||||||||||| || || ||||| | ||||| |||||||||| ||||||
Db    1081 CTTAAAGAAATGAAACTTCGTATCGAAGATGCCTTGAATGCCACACGTGCAGCTGTTGAA 1140

Qy    1233 GAAGGTATCGTTGCTGGTGGTGGAACAGCACTTATTACGGTTATTGAAAAAGTAGCAGCT 1292
           |||||||||||||||||||||||||||||||||||||||||||| || |||||||| |||
Db    1141 GAAGGTATCGTTGCTGGTGGTGGAACAGCACTTATTACGGTGATCGAAAAAGTAGCTGCT 1200

Qy    1293 CTTGAGCTTGAGGGCGATGATGCTACTGGACGTAACATTGTGCTTCGTGCTCTAGAAGAG 1352
           |||||||||| |||||||| |||||||| || || || || |||||||  | |||||
Db    1201 CTTGAGCTTGATGGCGATGACGCTACTGGCCGCAATATCGTTCTTCGTGCGTTGGAAGAA 1260
```

```
Qy   1353 CCTGTACGTCAAATTGCTTTAAATGCTGGGTACGAAGGCTCCGTAGTTATTGACAAGTTG 1412
          ||||| |||||||||||| || || ||||| |||||||| ||||| || || ||||| |||
Db   1261 CCTGTTCGTCAAATTGCATTCAACGCTGGTTACGAAGGTTCCGTTGTCATCGACAAATTG 1320

Qy   1413 AAAAACAGCCCTGCAGGAACAGGATTTAATGCTGCAACAGGTGAGTGGGTTGATATGATT 1472
          ||||| ||||||| |||||||| |||||||| ||||||||||||||||| |||||||||
Db   1321 AAAAATAGCCCTGTTGGAACAGGCTTTAATGCGGCAACAGGTGAGTGGGTAGATATGATT 1380

Qy   1473 AAAACAGGAATCATTGACCCTGTCAAAGTAACACGATCAGC 1513
               |||| || || || ||||| |||||||| || |||||
Db   1381 GCGGCAGGTATTATCGATCCTGTTAAAGTAACCCGTTCAGC 1421


RESULT 10
AX148809
LOCUS       AX148809               1305 bp    DNA     linear   PAT 08-JUN-2001
DEFINITION  Sequence 11 from Patent WO0136625.
ACCESSION   AX148809
VERSION     AX148809.1  GI:14347333
KEYWORDS    .
SOURCE      Streptococcus pyogenes.
  ORGANISM  Streptococcus pyogenes
            Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
            Streptococcus.
REFERENCE   1  (bases 1 to 1305)
  AUTHORS   Wright,J.A., Young,A.H. and Dugourd,D.
  TITLE     Antisense oligonucleotide sequences derived from groel and groes as
            inhibitors of microorganisms
  JOURNAL   Patent: WO 0136625-A 11 25-MAY-2001;
            GeneSense Technologies Inc. (CA)
FEATURES             Location/Qualifiers
     source          1. .1305
                     /organism="Streptococcus pyogenes"
                     /db_xref="taxon:1314"
BASE COUNT      406 a    238 c    312 g    349 t
ORIGIN

  Query Match           67.6%;  Score 1122.6;  DB 6;  Length 1305;
  Best Local Similarity   99.2%;  Pred. No. 5.9e-219;
  Matches 1128;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy    503 TATGGAGCGTGTGGGCAACGATGGTGTGATTACCATCGAAGAATCTCGAGGTATGGAAAC 562
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 TATGGAGCGTGTGGGCAACGATGGTGTGATTACCATCGAAGAATCTCGAGGTATGGAAAC 60

Qy    563 AGAACTTGAAGTGGTTGAAGGCATGCAATTTGACCGTGGTTACCTGTCTCAATACATGGT 622
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AGAACTTGAAGTGGTTGAAGGCATGCAATTTGACCGTGGTTACCTGTCTCAATACATGGT 120

Qy    623 CACAGACAATGAAAAAATGGTTGCAGACCTTGAAAACCCATTTATCTTAATCACGGATAA 682
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CACAGACAATGAAAAAATGGTTGCAGACCTTGAAAACCCATTTATCTTAATCACGGATAA 180

Qy    683 AAAAGTGTCAAACATCCAAGACATTTTGCCACTACTTGAGGAAGTTCTTAAAACCAACCG 742
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AAAAGTGTCAAACATCCAAGACATTTTGCCACTACTTGAGGAAGTTCTTAAAACCAACCG 240

Qy    743 TCCATTACTCATTATTGCAGATGATGTGGATGGTGAAGCACTTCCAACCCTTGTCTTGAA 802
          |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db    241 TCCATTACTCATTATTGCAGATGATGTGGATGGTGAAGCCCTTCCAACCCTTGTCTTGAA 300

Qy    803 CAAGATTCGTGGTACTTTCAATGTGGTTGCTGTCAAAGCGCCAGGATTTGGTGATCGTCG 862
          |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db    301 CAAGATTCGTGGTACTTTCAATGTGGTTGCTGTCAAAGCGCCAGGATTTGGTGATCGCCG 360

Qy    863 TAAAGCTATGCTTGAAGACATTGCTATCTTGACAGGTGGTACAGTGATTACAGAGGATCT 922
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 TAAAGCTATGCTTGAAGACATTGCTATCTTGACAGGTGGTACAGTGATTACAGAGGATCT 420

Qy    923 AGGACTTGAATTAAAAGATGCTACAATGACAGCCCTTGGACAGGCTGCTAAGATTACAGT 982
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AGGACTTGAATTAAAAGATGCTACAATGACAGCCCTTGGACAGGCTGCTAAGATTACAGT 480

Qy    983 TGATAAAGATAGCACAGTAATTGTTGAAGGTTCAGGAAGTTCAGAAGCTATTGCTAACCG 1042
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TGATAAAGATAGCACAGTAATTGTTGAAGGTTCAGGAAGTTCAGAAGCTATTGCTAACCG 540

Qy   1043 TATTGCACTGATTAAATCGCAATTAGAAACAACAACTTCTGACTTTGACCGTGAAAAACT 1102
          |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db    541 TATTGCACTGATTAAATCGCAATTAGAGACAACAACTTCTGACTTTGACCGTGAAAAACT 600

Qy   1103 ACAAGAACGTTTGGCGAAATTAGCTGGTGGTGTAGCTGTTATCAAAGTAGGAGCTCCAAC 1162
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 ACAAGAACGTTTGGCGAAATTAGCTGGTGGTGTAGCTGTTATCAAAGTAGGAGCTCCAAC 660

Qy   1163 AGAGACAGCTTTAAAAGAAATGAAACTTCGCATTGAGGATGCTCTAAATGCTACACGTGC 1222
          |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db    661 AGAGACAGCTTTAAAAGAAATGAAACTTCGCATTGAGGACGCTCTAAATGCTACACGTGC 720

Qy   1223 AGCCGTTGAAGAAGGTATCGTTGCTGGTGGTGGAACAGCACTTATTACGGTTATTGAAAA 1282
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AGCCGTTGAAGAAGGTATCGTTGCTGGTGGTGGAACAGCACTTATTACGGTTATTGAAAA 780

Qy   1283 AGTAGCAGCTCTTGAGCTTGAGGGCGATGATGCTACTGGACGTAACATTGTGCTTCGTGC 1342
          ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db    781 AGTAGCAGCTCTTGAACTTGAGGGCGATGATGCTACTGGACGTAACATTGTGCTTCGTGC 840

Qy   1343 TCTAGAAGAGCCTGTACGTCAAATTGCTTTAAATGCTGGGTACGAAGGCTCCGTAGTTAT 1402
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TCTAGAAGAGCCTGTACGTCAAATTGCTTTAAATGCTGGGTACGAAGGCTCCGTAGTTAT 900

Qy   1403 TGACAAGTTGAAAAACAGCCCTGCAGGAACAGGATTTAATGCTGCAACAGGTGAGTGGGT 1462
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 TGACAAGTTGAAAAACAGCCCTGCAGGAACAGGATTTAATGCTGCAACAGGTGAGTGGGT 960

Qy   1463 TGATATGATTAAAACAGGAATCATTGACCCTGTCAAAGTAACACGATCAGCGCTTCAAAA 1522
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 TGATATGATTAAAACAGGAATCATTGACCCTGTCAAAGTAACACGATCAGCGCTTCAAAA 1020

Qy   1523 TGCAGCTTCTGTAGCTAGTCTTATTTTGACAACAGAAGCAGTTGTTGCTAATAAACCTGA 1582
          |||||||||||||||||||| |||||||||||||||||||||||||||||||| |||||
Db    1021 TGCAGCTTCTGTAGCTAGTCTGATTTTGACAACAGAAGCAGTTGTTGCTAATAAGCCTGA 1080

Qy   1583 ACCAGCTACGCCAGCGCCAGCAATGCCAGCAGGTATGGATCCAGGAATGATGGGTGG 1639
          ||||||| ||||||||||||||||||||||||||||||||||||||||||||||| ||
Db    1081 ACCAGCTGCGCCAGCGCCAGCAATGCCAGCAGGTATGGATCCAGGAATGATGGGCGG 1137


RESULT 11
AY121367
LOCUS       AY121367               1415 bp    DNA     linear   BCT 30-JUL-2002
DEFINITION  Streptococcus dysgalactiae strain HKU 7 chaperonin GroEL gene,
            partial cds.
ACCESSION   AY121367
VERSION     AY121367.1  GI:22022493
KEYWORDS    .
SOURCE      Streptococcus dysgalactiae.
  ORGANISM  Streptococcus dysgalactiae
            Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
            Streptococcus.
REFERENCE   1  (bases 1 to 1415)
  AUTHORS   Woo,P.C.Y., Teng,J.L.L., Lau,S.K.P., Lum,P.N.L., Leung,K.-W.,
            Tse,H., Wong,K.-L., Li,K.-W., Lam,K.-C. and Yuen,K.-Y.
  TITLE     Chaperonin GroEL gene of Group G Streptococcus dysgalactiae
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1415)
  AUTHORS   Woo,P.C.Y., Teng,J.L.L., Lau,S.K.P., Lum,P.N.L., Leung,K.-W.,
            Tse,H., Wong,K.-L., Li,K.-W., Lam,K.-C. and Yuen,K.-Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-JUN-2002) Microbiology, The University of Hong Kong,
            Pokfulam Road, Hong Kong, China
FEATURES             Location/Qualifiers
     source          1. .1415
                     /organism="Streptococcus dysgalactiae"
                     /strain="HKU 7"
```

```
                     /db_xref="taxon:1334"
     CDS             <1. .>1415
                     /codon_start=3
                     /transl_table=11
                     /product="chaperonin GroEL"
                     /protein_id="AAM83130.1"
                     /db_xref="GI:22022494"
                     /translation="LGPKGRNVVLEKAFGSPLITNDGVTIAKEIELEDHFENMGAKLV
                     SEVASKTNDIAGDGTTTATVLTQAIVREGLKNVTAGANPIGIRRGIETATATAVEALK
                     AIAQPVSGKEAIAQVAAVSSRSEKVGEYISEAMERVGNDGVITIEESRGMETELEVVE
                     GMQFDRGYLSQYMVTDNEKMVADLENPFILITDKKVSNIQDILPLLEEVLKTNRPLLI
                     IADDVDGEALPTLVLNKIRGTFNVVAVKAPGFGDRRKAMLEDIAILTGGTVITEDLGL
                     ELKDATMPALGQAAKVTVDKDSTVIVEGAGSSEAIANRVGLIKSQLETTTSDFDREKL
                     QERLAKLAGGVAVIKVGAATETALKEMKLRIEDALNATRAAVEEGIVAGGGTALITVI
                     EKVAALELDGDDATGRNIVLRALEEPVRQIAFNAGYEGSVVIDKLKNSPVGTGFNAAT
                     GEWVDMIAAGIIDPVKVTRSA"
BASE COUNT      404 a    276 c    353 g    382 t
ORIGIN
```

Query Match 67.3%; Score 1118; DB 1; Length 1415;
Best Local Similarity 86.9%; Pred. No. 5.1e-218;
Matches 1229; Conservative 0; Mismatches 185; Indels 0; Gaps 0;

```
Qy    100 CGCTTGGTCCTAAAGGGCGCAATGTTGTTCTTGAAAAAGCTTTTGGTTCTCCCTTAATTA 159
Db      1 CGCTTGGTCCTAAAGGTCGTAACGTGGTTCTTGAAAAAGCTTTTGGATCTCCTTTGATTA 60

Qy    160 CTAATGACGGGGTAACCATTGCTAAAGAGATCGAATTAGAAGATCATTTTGAAAACATGG 219
Db     61 CCAATGACGGGGTTACCATTGCTAAAGAGATTGAATTAGAAGACCATTTTGAGAATATGG 120

Qy    220 GAGCAAAATTGGTGTCTGAAGTGGCTTCTAAAACCAATGATATTGCTGGTGATGGGACGA 279
Db    121 GAGCTAAATTGGTTTCTGAAGTTGCTTCTAAAACCAATGATATCGCAGGTGACGGAACCA 180

Qy    280 CTACTGCAACAGTTTTGACACAAGCCATTGTTCATGAAGGACTAAAAAATGTGACAGCAG 339
Db    181 CAACTGCAACAGTATTGACACAGGCTATCGTCCGTGAAGGGCTTAAAAATGTAACTGCTG 240

Qy    340 GTGCTAATCCAATTGGTATCCGTCGAGGCATTGAAACAGCAACAGCAACAGCTGTTGAAG 399
Db    241 GTGCCAACCCAATTGGTATTCGTCGTGGGATTGAAACAGCAACAGCAACAGCCGTTGAAG 300

Qy    400 CCTTGAAAGCCATTGCTCAACCTGTATCTGGCAAGGAAGCTATTGCTCAGGTCGCTGCAG 459
Db    301 CCTTGAAAGCTATTGCTCAGCCTGTTTCTGGTAAAGAAGCGATTGCTCAAGTTGCTGCTG 360

Qy    460 TATCATCACGCTCTGAAAAAGTTGGAGAGTATATCTCAGAAGCTATGGAGCGTGTGGGCA 519
Db    361 TGTCATCTCGTTCTGAAAAAGTTGGAGAATACATCTCAGAAGCCATGGAACGTGTGGGCA 420

Qy    520 ACGATGGTGTGATTACCATCGAAGAATCTCGAGGTATGGAAACAGAACTTGAAGTGGTTG 579
Db    421 ATGACGGTGTCATTACCATCGAAGAATCACGTGGTATGGAGACAGAGCTTGAAGTGGTAG 480

Qy    580 AAGGCATGCAATTTGACCGTGGTTACCTGTCTCAATACATGGTCACAGACAATGAAAAAA 639
Db    481 AAGGCATGCAGTTTGATCGTGGTTACCTGTCTCAATACATGGTCACAGACAATGAAAAAA 540

Qy    640 TGGTTGCAGACCTTGAAAACCCATTTATCTTAATCACGGATAAAAAAGTGTCAAACATCC 699
Db    541 TGGTTGCAGACCTTGAGAACCCATTTATCTTGATTACTGACAAAAAAGTGTCAAACATCC 600

Qy    700 AAGACATTTTGCCACTACTTGAGGAAGTTCTTAAAACCAACCGTCCATTACTCATTATTG 759
Db    601 AAGATATTCTCCCATTGCTTGAGGAAGTTCTTAAAACCAACCGTCCATTGTTGATTATCG 660

Qy    760 CAGATGATGTGGATGGTGAAGCACTTCCAACCCTTGTCTTGAACAAGATTCGTGGTACTT 819
Db    661 CCGATGACGTTGATGGCGAAGCTCTTCCAACCCTTGTTTTGAATAAAATTCGTGGTACTT 720

Qy    820 TCAATGTGGTTGCTGTCAAAGCGCCAGGATTTGGTGATCGTCGTAAAGCTATGCTTGAAG 879
Db    721 TCAATGTGGTTGCTGTCAAAGCTCCAGGATTTGGTGATCGCCGTAAAGCTATGCTTGAGG 780

Qy    880 ACATTGCTATCTTGACAGGTGGTACAGTGATTACAGAGGATCTAGGACTTGAATTAAAAG 939
Db    781 ATATCGCTATCTTGACAGGTGGTACAGTCATTACAGAAGACTTGGGTCTTGAATTGAAAG 840

Qy    940 ATGCTACAATGACAGCCCTTGGACAGGCTGCTAAGATTACAGTTGATAAAGATAGCACAG 999
Db    841 ACGCTACGATGCCAGCTCTTGGTCAAGCTGCTAAAGTGACTGTGGATAAAGACAGCACAG 900

Qy   1000 TAATTGTTGAAGGTTCAGGAAGTTCAGAAGCTATTGCTAACCGTATTGCACTGATTAAAT 1059
Db    901 TTATTGTGGAAGGTGCAGGAAGTTCTGAAGCCATTGCCAACCGTGTTGGCTTGATTAAGT 960

Qy   1060 CGCAATTAGAAACAACAACTTCTGACTTTGACCGTGAAAAACTACAAGAACGTTTGGCGA 1119
Db    961 CACAACTAGAAACCACAACGTCTGACTTTGACCGTGAAAAATTACAAGAACGCTTGGCGA 1020

Qy   1120 AATTAGCTGGTGGTGTAGCTGTTATCAAAGTAGGAGCTCCAACAGAGACAGCTTTAAAAG 1179
Db   1021 AATTAGCTGGTGGTGTGGCTGTCATCAAGGTAGGTGCTGCAACAGAAACAGCCCTTAAAG 1080

Qy   1180 AAATGAAACTTCGCATTGAGGATGCTCTAAATGCTACACGTGCAGCCGTTGAAGAAGGTA 1239
Db   1081 AAATGAAACTTCGTATCGAAGATGCCTTGAATGCCACACGTGCAGCCGTTGAAGAAGGTA 1140

Qy   1240 TCGTTGCTGGTGGTGGAACAGCACTTATTACGGTTATTGAAAAAGTAGCAGCTCTTGAGC 1299
Db   1141 TCGTTGCTGGTGGTGGAACAGCACTTATTACGGTGATCGAAAAAGTAGCTGCTCTTGAGC 1200

Qy   1300 TTGAGGGCGATGATGCTACTGGACGTAACATTGTGCTTCGTGCTCTAGAAGAGCCTGTAC 1359
Db   1201 TTGATGGCGATGACGCTACTGGCCGCAATATCGTTCTTCGTGCGTTAGAAGAACCTGTTC 1260

Qy   1360 GTCAAATTGCTTTAAATGCTGGGTACGAAGGCTCCGTAGTTATTGACAAGTTGAAAAACA 1419
Db   1261 GTCAAATTGCATTCAACGCTGGTTACGAAGGTTCCGTTGTCATCGACAAATTGAAAAATA 1320

Qy   1420 GCCCTGCAGGAACAGGATTTAATGCTGCAACAGGTGAGTGGGTTGATATGATTAAAACAG 1479
Db   1321 GCCCTGTTGGAACAGGCTTTAATGCGGCAACAGGTGAATGGGTAGATATGATTGCGGCAG 1380

Qy   1480 GAATCATTGACCCTGTCAAAGTAACACGATCAGC 1513
Db   1381 GTATTATCGATCCTGTTAAAGTAACCCGTTCAGC 1414
```

```
RESULT 12
AF389514
LOCUS       AF389514               2054 bp    DNA     linear   BCT 02-JUL-2002
DEFINITION  Streptococcus bovis GroES gene, complete cds; and GroEL gene,
            partial cds.
ACCESSION   AF389514
VERSION     AF389514.1  GI:21666288
KEYWORDS    .
SOURCE      Streptococcus bovis.
  ORGANISM  Streptococcus bovis
            Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
            Streptococcus.
REFERENCE   1  (bases 1 to 2054)
  AUTHORS   Teng,L.-J.
  TITLE     The groESL genes of Streptococcus bovis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2054)
  AUTHORS   Teng,L.-J.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-JUN-2001) School of Medical Technology, National
            Taiwan University College of Medicine, No. 1, Chang-Te Street,
            Taipei 100, Taiwan
FEATURES             Location/Qualifiers
     source          1. .2054
                     /organism="Streptococcus bovis"
                     /db_xref="taxon:1315"
```

```
     CDS             92. .376
                     /codon_start=1
                     /transl_table=11
                     /product="GroES"
                     /protein_id="AAM73641.1"
                     /db_xref="GI:21666289"
                     /translation="MLKPLGDRVVLKVEEEKEQTVGGFVLAGASKERTQVATVVAVGD
                     GARTLTGELVAPSVAAGDKVIIENGVGIEVKDDDNTVTIVREADILAILA"
     CDS             444. .>2054
                     /codon_start=1
                     /transl_table=11
                     /product="GroEL"
                     /protein_id="AAM73642.1"
                     /db_xref="GI:21666290"
                     /translation="MAKDIKFSADARASMMRGVDILADTVKVTLGPKGRNVVLEKSFG
                     SPLITNDGVTIAKEIELEDHFENMGAKLVSEVASKTNDIAGDGTTTATVLTQAIVREG
                     LKNVTAGANPIGIRRGIESAVAVAVDELKAIAQPVANKEAIAQVAAVSSRSEKVGEYI
                     SEAMEKVGNDGVITIEESRGMETELDVVEGMQFDRGYLSQYMVTDNEKMVADLENPYI
                     LITDKKISNIQDILPLLEEVLKTSRPLLIIADDVDGEALPTLVLNKIRGTFNVVAVKA
                     PGFGDRRKAMLEDIAVLTGGTVITEDLGLDLKDANMTALGQAAKVTVDKDSTVIVEGA
                     GEASSIANRVNVIKSQLEATTSEFDREKLQERLAKLAGGVAVIKVGAATETELKEMKL
                     RIEDALNATRAAVEEGIVAGGGTALVNVISKVAELELDGDEATGRNIVLRALEEPVRQ
                     IAFNAGYEGSVIIEHLKNSEVGTGFNAANGEWVNMVEAGIIDPVKVTRSALQNAASVA
                     SLILTTEAVVANHPEPAAPAPAAPGMDPS"
BASE COUNT      652 a    361 c    472 g    569 t
ORIGIN

  Query Match           66.5%;  Score 1104.2;  DB 1;  Length 2054;
  Best Local Similarity  80.7%;  Pred. No. 3.1e-215;
  Matches 1289;  Conservative    0;  Mismatches  308;  Indels    0;  Gaps    0;

Qy      15 ATGGCAAAAGAAATCAAATTTTCAGCAGATGCGCGTGCTGCCATGGTGCGCGGAGTTGAT 74
           |||||||||||| || ||||||||||||||||||| |||||   |||| |||| || || |||
Db     444 ATGGCAAAAGATATTAAATTTTCAGCAGATGCACGTGCAAGCATGATGCGTGGTGTGGAT 503

Qy      75 ATGTTAGCAGATACCGTCAAAGTAACGCTTGGTCCTAAAGGGCGCAATGTTGTTCTTGAA 134
           || || |||||||||||| ||||||||  | || |||||||| || || || ||||||||||
Db     504 ATTTTGGCAGATACCGTTAAAGTAACCTTAGGCCCTAAAGGTCGTAACGTGGTTCTTGAA 563

Qy     135 AAAGCTTTTGGTTCTCCCTTAATTACTAATGACGGGGTAACCATTGCTAAAGAGATCGAA 194
           ||| | ||||||||| ||  | || || ||||| || || || || || ||||| ||||||
Db     564 AAATCATTTGGTTCACCACTTATCACAAATGATGGTGTGACAATCGCCAAAGAAATCGAA 623

Qy     195 TTAGAAGATCATTTTGAAAACATGGGAGCAAAATTGGTGTCTGAAGTGGCTTCTAAAACC 254
           |||||||| |||||||||||| ||||||| ||| | || || ||||| ||||| |||||
Db     624 TTAGAAGACCATTTTGAAAATATGGGAGCTAAACTTGTATCAGAAGTTGCTTCAAAAACA 683

Qy     255 AATGATATTGCTGGTGATGGGACGACTACTGCAACAGTTTTGACACAAGCCATTGTTCAT 314
           || || || |||||||| || ||||| ||||| ||||| |||||||||||| || |||| |
Db     684 AACGACATCGCTGGTGACGGTACGACAACTGCCACAGTATTGACACAAGCTATCGTTCGT 743

Qy     315 GAAGGACTAAAAAATGTGACAGCAGGTGCTAATCCAATTGGTATCCGTCGAGGCATTGAA 374
           ||||| || ||||| || || || ||||| || |||||||||||||||||| || || |||
Db     744 GAAGGTCTTAAAAACGTTACTGCGGGTGCAAACCCAATTGGTATCCGTCGTGGTATCGAA 803

Qy     375 ACAGCAACAGCAACAGCTGTTGAAGCCTTGAAAGCCATTGCTCAACCTGTATCTGGCAAG 434
           ||||    ||    || ||||| |  |||||||| |||||||||| ||  ||   ||
Db     804 TCAGCTGTCGCTGTTGCAGTTGACGAATTGAAAGCTATTGCTCAACCAGTTGCTAATAAA 863

Qy     435 GAAGCTATTGCTCAGGTCGCTGCAGTATCATCACGCTCTGAAAAAGTTGGAGAGTATATC 494
           ||||| |||||||| || ||||| || |||||||| |||||||||||||| || || ||
Db     864 GAAGCGATTGCTCAAGTTGCTGCGGTTTCATCACGTTCTGAAAAAGTTGGTGAATACATT 923

Qy     495 TCAGAAGCTATGGAGCGTGTGGGCAACGATGGTGTGATTACCATCGAAGAATCTCGAGGT 554
           ||||||||||||||    || |||||||| ||||| || || |||||||||| || |||
Db     924 TCAGAAGCTATGGAAAAAGTTGGCAACGACGGTGTTATCACTATCGAAGAATCACGTGGT 983

Qy     555 ATGGAAACAGAACTTGAAGTGGTTGAAGGCATGCAATTTGACCGTGGTTACCTGTCTCAA 614
           |||||||||||||||| || |||||||| ||||||||||||||||||||| || || |||
Db     984 ATGGAAACAGAACTTGACGTTGTTGAAGGTATGCAATTTGACCGTGGTTATCTTTCACAA 1043

Qy     615 TACATGGTCACAGACAATGAAAAAATGGTTGCAGACCTTGAAAACCCATTTATCTTAATC 674
           |||||||| || ||||||||||||||||||| |||||||||| ||||  ||||| ||
Db    1044 TACATGGTTACTGACAATGAAAAAATGGTTGCTGACCTTGAAAATCCATACATCTTGATT 1103

Qy     675 ACGGATAAAAAAGTGTCAAACATCCAAGACATTTTGCCACTACTTGAGGAAGTTCTTAAA 734
           || ||||| ||| | |||||||| |||||||||||||||||| ||||| ||||| ||||||
Db    1104 ACAGATAAGAAAATCTCAAACATTCAAGACATTTTGCCACTTCTTGAAGAAGTGCTTAAA 1163

Qy     735 ACCAACCGTCCATTACTCATTATTGCAGATGATGTGGATGGTGAAGCACTTCCAACCCTT 794
           || |  |||||| | || |||||||| |||||||| || |||||||| |||||||| |||
Db    1164 ACTAGTCGTCCACTTCTTATTATTGCTGATGATGTTGACGGTGAAGCTCTTCCAACACTT 1223

Qy     795 GTCTTGAACAAGATTCGTGGTACTTTCAATGTGGTTGCTGTCAAAGCGCCAGGATTTGGT 854
           ||  | ||||| |||||||||||||||||| || || ||||| || || || |||||||||
Db    1224 GTGCTTAACAAAATTCGTGGTACTTTCAACGTTGTAGCTGTTAAGGCTCCTGGATTTGGT 1283

Qy     855 GATCGTCGTAAAGCTATGCTTGAAGACATTGCTATCTTGACAGGTGGTACAGTGATTACA 914
           || |||||||||||| |||||||||||  | || || |||||||| || || ||| |||||
Db    1284 GACCGTCGTAAAGCAATGCTTGAAGATATTGCCGTTTTAACTGGTGGTACTGTCATCACA 1343

Qy     915 GAGGATCTAGGACTTGAATTAAAAGATGCTACAATGACAGCCCTTGGACAGGCTGCTAAG 974
           || || || || ||||| || |||||||| |  |||||||| |||||||| |||||||||
Db    1344 GAAGACCTTGGTCTTGATTTGAAAGATGCCAACATGACAGCTCTTGGACAAGCTGCTAAA 1403

Qy     975 ATTACAGTTGATAAAGATAGCACAGTAATTGTTGAAGGTTCAGGAAGTTCAGAAGCTATT 1034
           | || |||||||||||||| ||||| |||||||||| | ||      |  | ||||
Db    1404 GTAACTGTTGATAAAGATAGTACAGTTATTGTTGAAGGAGCTGGTGAGGCTTCATCTATC 1463

Qy    1035 GCTAACCGTATTGCACTGATTAAATCGCAATTAGAAACAACAACTTCTGACTTTGACCGT 1094
           ||||| |||| |     |||||||||| ||| | ||| ||||||| || || |||||||||
Db    1464 GCTAATCGTGTCAATGTGATTAAATCACAACTCGAAGCAACAACATCAGAATTTGACCGT 1523

Qy    1095 GAAAAACTACAAGAACGTTTGGCGAAATTAGCTGGTGGTGTAGCTGTTATCAAAGTAGGA 1154
           |||||| |||||||||||||||| |||||||||||||| |||||||||||||||||| ||
Db    1524 GAAAAATTACAAGAACGTTTGGCTAAATTAGCTGGTGGAGTAGCTGTTATCAAAGTTGGT 1583

Qy    1155 GCTCCAACAGAGACAGCTTTAAAAGAAATGAAACTTCGCATTGAGGATGCTCTAAATGCT 1214
           ||  | ||||| ||||  || |||||||||||| | || ||||| ||||| || |||||
Db    1584 GCAGCGACAGAAACAGAATTGAAAGAAATGAAATTGCGTATTGAAGATGCGCTTAATGCC 1643

Qy    1215 ACACGTGCAGCCGTTGAAGAAGGTATCGTTGCTGGTGGTGGAACAGCACTTATTACGGTT 1274
           ||||| || |||||||||||||||||| ||||| |||||||| |||||||| | |  ||
Db    1644 ACACGCGCTGCCGTTGAAGAAGGTATTGTTGCAGGTGGTGGTACAGCACTTGTCAATGTC 1703

Qy    1275 ATTGAAAAAGTAGCAGCTCTTGAGCTTGAGGGCGATGATGCTACTGGACGTAACATTGTG 1334
           |||  |||||| || |  ||||| |||||| || ||||| || || || ||||||||||
Db    1704 ATTTCAAAAGTTGCTGAACTTGAACTTGACGGTGATGAAGCAACAGGTCGTAACATTGTT 1763

Qy    1335 CTTCGTGCTCTAGAAGAGCCTGTACGTCAAATTGCTTTAAATGCTGGGTACGAAGGCTCC 1394
           |||||||||||| ||||| || || |||||||||| || |||||||| |||||||| ||
Db    1764 CTTCGTGCTCTTGAAGAACCAGTTCGTCAAATTGCATTCAATGCTGGTTACGAAGGTTCA 1823

Qy    1395 GTAGTTATTGACAAGTTGAAAAACAGCCCTGCAGGAACAGGATTTAATGCTGCAACAGGT 1454
           ||  | || ||  | |||||||||       |  || |||||||||| ||||| |  |||
Db    1824 GTTATCATCGAACACTTGAAAAACTCAGAAGTTGGTACAGGATTTAACGCTGCCAACGGT 1883

Qy    1455 GAGTGGGTTGATATGATTAAAACAGGAATCATTGACCCTGTCAAAGTAACACGATCAGCG 1514
           || |||||  | ||| || || |||| ||||||||||||||| ||||||||||| |||||
Db    1884 GAATGGGTAAACATGGTTGAAGCAGGTATCATTGACCCTGTTAAAGTAACACGTTCAGCC 1943
                                                    i
Qy    1515 CTTCAAAATGCAGCTTCTGTAGCTAGTCTTATTTTGACAACAGAAGCAGTTGTTGCTAAT 1574
           |||||||||||| || || || || |||||||||||||||||| ||||| ||||| ||||||
Db    1944 CTTCAAAATGCCGCGTCAGTTGCAAGTCTTATTTTGACAACTGAAGCCGTTGTGGCTAAT 2003

Qy    1575 AAACCTGAACCAGCTACGCCAGCGCCAGCAATGCCAG 1611
           |  || |||||||||  | ||||||||||||   ||||
Db    2004 CATCCAGAACCAGCTGCACCAGCGCCAGCAGCTCCAG 2040


RESULT 13
AY121363
LOCUS       AY121363               1384 bp    DNA     linear   BCT 30-JUL-2002
DEFINITION  Streptococcus dysgalactiae subsp. dysgalactiae strain ATCC 43078
            chaperonin GroEL gene, partial cds.
ACCESSION   AY121363
```

```
VERSION     AY121363.1  GI:22022485
KEYWORDS    .
SOURCE      Streptococcus dysgalactiae subsp. dysgalactiae.
  ORGANISM  Streptococcus dysgalactiae subsp. dysgalactiae
            Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
            Streptococcus.
REFERENCE   1  (bases 1 to 1384)
  AUTHORS   Woo,P.C.Y., Teng,J.L.L., Lau,S.K.P., Lum,P.N.L., Leung,K.-W.,
            Tse,H., Wong,K.-L., Li,K.-W., Lam,K.-C. and Yuen,K.-Y.
  TITLE     Chaperonin GroEL gene of Group C Streptococcus dysgalactiae
            subspecies dysgalactiae
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1384)
  AUTHORS   Woo,P.C.Y., Teng,J.L.L., Lau,S.K.P., Lum,P.N.L., Leung,K.-W.,
            Tse,H., Wong,K.-L., Li,K.-W., Lam,K.-C. and Yuen,K.-Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-JUN-2002) Microbiology, The University of Hong Kong,
            Pokfulam Road, Hong Kong, China
FEATURES             Location/Qualifiers
     source          1. .1384
                     /organism="Streptococcus dysgalactiae subsp. dysgalactiae"
                     /strain="ATCC 43078"
                     /sub_species="dysgalactiae"
                     /db_xref="ATCC:43078"
                     /db_xref="taxon:99822"
     CDS             <1. .>1384
                     /codon_start=3
                     /transl_table=11
                     /product="chaperonin GroEL"
                     /protein_id="AAM83126.1"
                     /db_xref="GI:22022486"
                     /translation="NVVLEKAFGSPLITNDGVTIAKEIELEDHFENMGAKLVSEVASK
                     TNDIAGDGTTTATVLTQAIVREGLKNVTAGANPIGIRRGIETATATAVEALKAIAQPV
                     SGKEAIAQVAAVSSRSEKVGEYISEAMERVGNDGVITIEESRGMETELEVVEGMQFDR
                     GYLSQYMVTDNEKMVADLENPFILITDKKVSNIQDILPLLEEVLKTNRPLLIIADDVD
                     GEALPTLVLNKIRGTFNVVAVKAPGFGDRRKAMLEDIAILTGGTVITEDLGLELKDAT
                     MPALGQAAKVTVDKDSTVIVEGAGSSEAIANRVGLIKSQLETTTSDFDREKLQERLAK
                     LAGGVAVIKVGAATETALKEMKLRIEDALNATRAAVEEGIVAGGGTALITAIEKVAAL
                     ELDGDDATGRNIVLRALEEPVRQIAFNAGYEGSVVIDKLKNSPVGTGFNAATGEWVDM
                     IAAGIIDPVKV"
BASE COUNT     397 a    269 c    349 g    369 t
ORIGIN
```

Query Match 65.0%; Score 1080; DB 1; Length 1384;
Best Local Similarity 86.3%; Pred. No. 2.9e-210;
Matches 1194; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

```
Qy    118 GCAATGTTGTTCTTGAAAAAGCTTTTGGTTCTCCCTTAATTACTAATGACGGGGGTAACCA 177
Db      1 GTAATGTGGTTCTTGAAAAAGCTTTTGGGTCTCCTTTGATTACCAATGACGGGGTTACCA 60

Qy    178 TTGCTAAAGAGATCGAATTAGAAGATCATTTTGAAAACATGGGAGCAAAATTGGTGTCTG 237
Db     61 TTGCTAAAGAGATTGAATTAGAAGACCATTTTGAGAATATGGGAGCTAAATTGGTTTCTG 120

Qy    238 AAGTGGCTTCTAAAACCAATGATATTGCTGGTGATGGGACGACTACTGCAACAGTTTTGA 297
Db    121 AAGTTGCTTCTAAAACTAACGATATCGCAGGTGACGGAACCACAACTGCAACAGTATTGA 180

Qy    298 CACAAGCCATTGTTCATGAAGGACTAAAAAATGTGACAGCAGGTGCTAATCCAATTGGTA 357
Db    181 CACAAGCTATCGTCCGTGAAGGGCTTAAAAATGTAACTGCTGGTGCCAACCCAATTGGCA 240

Qy    358 TCCGTCGAGGCATTGAAACAGCAACAGCAACAGCTGTTGAAGCCTTGAAAGCCATTGCTC 417
Db    241 TTCGTCGTGGGATTGAAACAGCAACAGCAACAGCCGTTGAAGCCTTGAAAGCGATTGCTC 300

Qy    418 AACCTGTATCTGGCAAGGAAGCTATTGCTCAGGTCGCTGCAGTATCATCACGCTCTGAAA 477
Db    301 AGCCTGTTTCTGGTAAAGAAGCCATTGCTCAAGTTGCTGCTGTGTCATCTCGTTCTGAAA 360

Qy    478 AAGTTGGAGAGTATATCTCAGAAGCTATGGAGCGTGTGGGCAACGATGGTGTGATTACCA 537
Db    361 AAGTTGGAGAATACATTTCAGAAGCCATGGAACGTGTGGGTAATGACGGTGTCATTACTA 420

Qy    538 TCGAAGAATCTCGAGGTATGGAAACAGAACTTGAAGTGGTTGAAGGCATGCAATTTGACC 597
Db    421 TCGAAGAATCACGTGGTATGGAGACAGAGCTTGAAGTGGTAGAAGGCATGCAGTTTGACC 480

Qy    598 GTGGTTACCTGTCTCAATACATGGTCACAGACAATGAAAAAATGGTTGCAGACCTTGAAA 657
Db    481 GTGGTTACCTGTCTCAATACATGGTCACAGACAATGAAAAAATGGTTGCCGACCTTGAGA 540

Qy    658 ACCCATTTATCTTAATCACGGATAAAAAAGTGTCAAACATCCAAGACATTTTGCCACTAC 717
Db    541 ACCCATTTATCTTGATTACTGACAAAAAAGTGTCAAACATCCAAGACATTCTTCCATTGC 600

Qy    718 TTGAGGAAGTTCTTAAAACCAACCGTCCATTACTCATTATTGCAGATGATGTGGATGGTG 777
Db    601 TTGAGGAAGTTCTTAAAACCAACCGTCCATTGTTGATTATCGCCGATGACGTTGATGGCG 660

Qy    778 AAGCACTTCCAACCCTTGTCTTGAACAAGATTCGTGGTACTTTCAATGTGGTTGCTGTCA 837
Db    661 AAGCTCTTCCAACCCTTGTTTTGAATAAAATTCGTGGTACTTTCAATGTGGTTGCTGTCA 720

Qy    838 AAGCGCCAGGATTTGGTGATCGTCGTAAAGCTATGCTTGAAGACATTGCTATCTTGACAG 897
Db    721 AAGCTCCAGGATTTGGTGATCGCCGTAAAGCCATGCTTGAGGACATCGCTATCTTGACAG 780

Qy    898 GTGGTACAGTGATTACAGAGGATCTAGGACTTGAATTAAAAGATGCTACAATGACAGCCC 957
Db    781 GTGGTACAGTCATTACAGAAGACTTAGGTCTTGAGTTGAAAGACGCTACGATGCCAGCTC 840

Qy    958 TTGGACAGGCTGCTAAGATTACAGTTGATAAAGATAGCACAGTAATTGTTGAAGGTTCAG 1017
Db    841 TTGGTCAAGCCGCTAAAGTGACTGTGGATAAAGACAGCACAGTTATTGTGGAAGGTGCAG 900

Qy   1018 GAAGTTCAGAAGCTATTGCTAACCGTATTGCACTGATTAAATCGCAATTAGAAACAACAA 1077
Db    901 GAAGTTCCGAAGCCATAGCCAACCGTGTTGGCTTGATTAAGTCACAACTGGAAACCACAA 960

Qy   1078 CTTCTGACTTTGACCGTGAAAAACTACAAGAACGTTTGGCGAAATTAGCTGGTGGTGTAG 1137
Db    961 CGTCTGACTTTGACCGTGAAAAATTACAAGAACGCTTGGCGAAATTAGCTGGTGGTGTGG 1020

Qy   1138 CTGTTATCAAAGTAGGAGCTCCAACAGAGACAGCTTTAAAAGAAATGAAACTTCGCATTG 1197
Db   1021 CTGTCATCAAGGTAGGTGCTGCAACAGAAACAGCCCTTAAAGAAATGAAACTTCGTATAG 1080

Qy   1198 AGGATGCTCTAAATGCTACACGTGCAGCCGTTGAAGAAGGTATCGTTGCTGGTGGTGGAA 1257
Db   1081 AAGACGCTTTGAATGCCACACGTGCAGCCGTTGAAGAAGGGATCGTTGCTGGTGGTGGAA 1140

Qy   1258 CAGCACTTATTACGGTTATTGAAAAAGTAGCAGCTCTTGAGCTTGAGGGCGATGATGCTA 1317
Db   1141 CAGCACTTATTACGGCAATCGAAAAAGTAGCTGCTCTTGAGCTTGATGGCGATGATGCTA 1200

Qy   1318 CTGGACGTAACATTGTGCTTCGTGCTCTAGAAGAGCCTGTACGTCAAATTGCTTTAAATG 1377
Db   1201 CTGGCCGCAATATCGTTCTTCGTGCGTTGGAAGAACCTGTTCGTCAAATTGCATTCAACG 1260

Qy   1378 CTGGGTACGAAGGCTCCGTAGTTATTGACAAGTTGAAAAACAGCCCTGCAGGAACAGGAT 1437
Db   1261 CTGGTTACGAAGGTTCCGTTGTCATCGACAAATTGAAAAATAGCCCTGTTGGAACAGGCT 1320

Qy   1438 TTAATGCTGCAACAGGTGAGTGGGTTGATATGATTAAAACAGGAATCATTGACCCTGTCA 1497
Db   1321 TTAATGCGGCAACAGGTGAGTGGGTAGACATGATTGCGGCAGGTATTATCGATCCTGTTA 1380

Qy   1498 AAGT 1501
Db   1381 AAGT 1384
```

RESULT 14
AF389516

```
LOCUS       AF389516               2324 bp    DNA     linear   BCT 02-JUL-2002
DEFINITION  Streptococcus mutans GroES gene, complete cds; and GroEL gene,
            partial cds.
ACCESSION   AF389516
VERSION     AF389516.1  GI:21666294
KEYWORDS    .
SOURCE      Streptococcus mutans.
  ORGANISM  Streptococcus mutans
            Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
            Streptococcus.
REFERENCE   1  (bases 1 to 2324)
  AUTHORS   Teng,L.-J.
  TITLE     The groESL genes of Streptococcus mutans
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2324)
  AUTHORS   Teng,L.-J.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-JUN-2001) School of Medical Technology, National
            Taiwan University College of Medicine, No. 1, Chang-Te Street,
            Taipei 100, Taiwan
FEATURES             Location/Qualifiers
     source          1. .2324
                     /organism="Streptococcus mutans"
                     /db_xref="taxon:1309"
     CDS             318. .605
                     /codon_start=1
                     /transl_table=11
                     /product="GroES"
                     /protein_id="AAM73645.1"
                     /db_xref="GI:21666295"
                     /translation="MLKPLGDRVVVQLKEEKEQTVGGFVLAGASQEKTKKAQVVAVGE
                     GVRTLTGELVASSLAQGDTILIENHVGTPVKDDGKDYLIIREADVLAVVND"
     CDS             717. .>2324
                     /codon_start=1
                     /transl_table=11
                     /product="GroEL"
                     /protein_id="AAM73646.1"
                     /db_xref="GI:21666296"
                     /translation="MAKDIKFSADARSSMVRGVDILADTVKVTLGPKGRNVVLEKSFG
                     SPLITNDGVTIAKEIELEDHFENMGAKLVSEVASKTNDIAGDGTTTATVLTQAIVREG
                     LKNVTAGANPIGIRRGIETAVATAVDELKAIAQPVSGKEAIAQVAAVSSRSEKVGEYV
                     SEAMEKVGNDGVITIEESRGMETELDVVEGMQFDRGYLSQYMVTDNEKMVADLENPYL
                     LITDKKISNIQDVLPLLEEVLKTNRPLLIIADDVDGEALPTLVLNKIRGTFNVVAVKA
                     PGFGDRRKAMLEDIAVLTGGTVITEDLGLELKDTTIDALGQAARVTVDKDSTVIVEGS
                     GGKEAVANRVNLIKSQIETATSDFDREKLQERLAKLSGGVAVIKVGAATETELKEMKL
                     RIEDALNATRAAVEEGIVAGGGTALINVIEKVAALDLTDDAATGRNLVLRALEEPVRQ
                     IAKNAGYEGSVIIDKLKNSSAGTGFNAANGEWVDMIDAGIIDPVKVTRSALQNAASVA
                     SLILTTEAVVADHPAPEAPAAAPAMDPS"
BASE COUNT      695 a    368 c    544 g    717 t
ORIGIN
```

```
  Query Match           64.8%;  Score 1076.4;  DB 1;  Length 2324;
  Best Local Similarity  79.8%;  Pred. No. 1.4e-209;
  Matches 1269;  Conservative    0;  Mismatches  321;  Indels    0;  Gaps    0;

Qy      14 TATGGCAAAAGAAATCAAATTTTCAGCAGATGCGCGTGCTGCCATGGTGCGCGGAGTTGA 73
           ||||||||||||| || ||||||||||||||||||  |       |||||||| || |||||
Db     716 TATGGCAAAAGATATTAAATTTTCAGCAGATGCAAGAAGCAGTATGGTGCGTGGTGTTGA 775

Qy      74 TATGTTAGCAGATACCGTCAAAGTAACGCTTGGTCCTAAAGGGCGCAATGTTGTTCTTGA 133
           ||| |||||||||||| || || |||||  | || ||||||||| ||||||||||||||||
Db     776 TATTTTAGCAGATACAGTTAAGGTAACCTTGGGCCCTAAAGGACGCAATGTTGTTCTTGA 835

Qy     134 AAAAGCTTTTGGTTCTCCCTTAATTACTAATGACGGGGTAACCATTGCTAAAGAGATCGA 193
           |||  | ||||||||| ||  | |||||||||| || || ||||| ||||| || || ||
Db     836 AAAGTCGTTTGGTTCACCGCTCATTACTAATGATGGTGTGACCATCGCTAAGGAAATTGA 895

Qy     194 ATTAGAAGATCATTTTGAAAACATGGGAGCAAAATTGGTGTCTGAAGTGGCTTCTAAAAC 253
           |||||||||||| |||||||| |||||||| ||| | || || || || ||||||||||
Db     896 ATTAGAAGATCACTTTGAAAATATGGGAGCTAAACTAGTTTCAGAGGTTGCTTCTAAAAC 955

Qy     254 CAATGATATTGCTGGTGATGGGACGACTACTGCAACAGTTTTGACACAAGCCATTGTTCA 313
           ||||||||||| |||||||||| || || || || || || || || || |||||||
Db     956 TAATGATATTGCCGGTGATGGGACAACGACAGCGACTGTGTTAACTCAGGCTATTGTTCG 1015

Qy     314 TGAAGGACTAAAAAATGTGACAGCAGGTGCTAATCCAATTGGTATCCGTCGAGGCATTGA 373
           ||||||  | |||||||||||| || || ||||| ||||| ||||| |||||||| || ||
Db    1016 TGAAGGTTTGAAAAATGTGACTGCTGGAGCTAACCCAATCGGTATTCGTCGAGGAATCGA 1075

Qy     374 AACAGCAACAGCAACAGCTGTTGAAGCCTTGAAAGCCATTGCTCAACCTGTATCTGGCAA 433
           |||||||  |||||||| ||||| |  |||||||| ||||| || ||||| ||||||||
Db    1076 AACAGCAGTTGCAACAGCAGTTGATGAGTTGAAAGCTATTGCACAGCCTGTTTCTGGCAA 1135

Qy     434 GGAAGCTATTGCTCAGGTCGCTGCAGTATCATCACGCTCTGAAAAAGTTGGAGAGTATAT 493
           |||||||||||| ||||| || || || |||||||| |||||||||||||| || ||  |
Db    1136 AGAAGCTATTGCACAGGTTGCAGCCGTTTCATCACGTTCTGAAAAAGTTGGGGAATACGT 1195

Qy     494 CTCAGAAGCTATGGAGCGTGTGGGCAACGATGGTGTGATTACCATCGAAGAATCTCGAGG 553
           || |||||||||||     || || |||||||||||| || || || |||||||||| ||
Db    1196 TTCTGAAGCTATGGAAAAAGTTGGTAACGATGGTGTTATCACTATTGAAGAATCTCGTGG 1255

Qy     554 TATGGAAACAGAACTTGAAGTGGTTGAAGGCATGCAATTTGACCGTGGTTACCTGTCTCA 613
           |||||||||||| ||||| || |||||||| |||||||||| || || ||||| || ||
Db    1256 TATGGAAACAGAGCTTGATGTTGTTGAAGGAATGCAATTTGATCGCGGCTACCTTTCCCA 1315

Qy     614 ATACATGGTCACAGACAATGAAAAAATGGTTGCAGACCTTGAAAACCCATTTATCTTAAT 673
           ||| ||||| || |||||||||||||||| ||||| |||||||| || | | | |||||
Db    1316 ATATATGGTAACTGACAATGAAAAAATGGTGGCAGATCTTGAAAATCCTTATTTGTTAAT 1375

Qy     674 CACGGATAAAAAAGTGTCAAACATCCAAGACATTTTGCCACTACTTGAGGAAGTTCTTAA 733
           || |||| ||| | |||| || |||||  || | || || || || ||||||||||||
Db    1376 TACAGATAAGAAAATTTCAAATATTCAAGATGTTCTTCCGCTTCTAGAAGAAGTTCTTAA 1435

Qy     734 AACCAACCGTCCATTACTCATTATTGCAGATGATGTGGATGGTGAAGCACTTCCAACCCT 793
           || |||||||  |  | |||||||| |||||||| |||||||||| || |||||  ||
Db    1436 GACAAACCGTCCTCTTTTAATTATTGCGGATGATGTAGATGGTGAAGCTCTCCCAACGCT 1495

Qy     794 TGTCTTGAACAAGATTCGTGGTACTTTCAATGTGGTTGCTGTCAAAGCGCCAGGATTTGG 853
           ||| ||||| |||||||||||||||||||||||| || || ||||| || || || || ||
Db    1496 TGTTTTGAATAAGATTCGTGGTACTTTCAATGTTGTCGCAGTCAAGGCTCCTGGTTTCGG 1555

Qy     854 TGATCGTCGTAAAGCTATGCTTGAAGACATTGCTATCTTGACAGGTGGTACAGTGATTAC 913
           ||||||||| || || |||||||||||| |||||| | || ||||| ||||| || |||||
Db    1556 TGATCGTCGCAAGGCCATGCTTGAAGATATTGCTGTTTTAACAGGGGGTACTGTTATTAC 1615

Qy     914 AGAGGATCTAGGACTTGAATTAAAAGATGCTACAATGACAGCCCTTGGACAGGCTGCTAA 973
           || ||||| || || ||||| |||||| | || ||    ||  | || || || |||
Db    1616 TGAAGATCTTGGTCTAGAATTGAAAGATACGACTATTGATGCGTTGGGTCAAGCAGCTCG 1675

Qy     974 GATTACAGTTGATAAAGATAGCACAGTAATTGTTGAAGGTTCAGGAAGTTCAGAAGCTAT 1033
           | || |||||||||||||    || || ||||||||||||||| ||  ||   |||||| |
Db    1676 TGTGACTGTTGATAAAGATTCAACTGTTATTGTTGAAGGTTCTGGCGGTAAGGAAGCTGT 1735

Qy    1034 TGCTAACCGTATTGCACTGATTAAATCGCAATTAGAAACAACAACTTCTGACTTTGACCG 1093
           |||||| ||| |    || ||||| || ||| | |||||| ||||||| |||||||| ||
Db    1736 TGCTAATCGTGTCAATCTCATTAAGTCTCAAATTGAAACAGCAACTTCAGACTTTGATCG 1795

Qy    1094 TGAAAAACTACAAGAACGTTTGGCGAAATTAGCTGGTGGTGTAGCTGTTATCAAAGTAGG 1153
           ||||||| |||||||||||||||| |||||| |||| ||||| || || |||||||| ||
Db    1796 TGAAAAATTACAAGAACGTTTGGCTAAATTATCTGGAGGTGTTGCCGTCATCAAAGTTGG 1855

Qy    1154 AGCTCCAACAGAGACAGCTTTAAAAGAAATGAAACTTCGCATTGAGGATGCTCTAAATGC 1213
           ||  ||||||| |||| || ||||||||||||||||||||||| ||||| || |||||
Db    1856 CGCAGCAACAGAAACAGAATTGAAAGAAATGAAACTTCGCATTGAAGATGCGCTTAATGC 1915

Qy    1214 TACACGTGCAGCCGTTGAAGAAGGTATCGTTGCTGGTGGTGGAACAGCACTTATTACGGT 1273
           ||| || ||||| || |||||||| || ||||| |||||||||| |||||||| |  ||
Db    1916 TACTCGAGCAGCTGTAGAAGAAGGAATTGTTGCAGGTGGTGGAACGGCACTTATCAATGT 1975

Qy    1274 TATTGAAAAAGTAGCAGCTCTTGAGCTTGAGGGCGATGATGCTACTGGACGTAACATTGT 1333
           |||||||||||||||||| ||||  |    | |||| ||| || || || || ||||
Db    1976 TATTGAAAAAGTAGCAGCACTTGATTTAACAGATGATGCTGCAACAGGTCGCAATCTTGT 2035

Qy    1334 GCTTCGTGCTCTAGAAGAGCCTGTACGTCAAATTGCTTTAAATGCTGGGTACGAAGGCTC 1393
           || |||||||| |||||||||| |||||||||||  |||||||| || ||||||||
Db    2036 TCTGCGTGCTCTTGAAGAGCCTGTCCGTCAAATTGCTAAAAATGCTGGTTATGAAGGCTC 2095
```

```
Qy   1394 CGTAGTTATTGACAAGTTGAAAAACAGCCCTGCAGGAACAGGATTTAATGCTGCAACAGG 1453
Db   2096 TGTCATTATTGATAAATTGAAGAACAGTTCAGCAGGTACAGGTTTCAATGCTGCTAACGG 2155

Qy   1454 TGAGTGGGTTGATATGATTAAAACAGGAATCATTGACCCTGTCAAAGTAACACGATCAGC 1513
Db   2156 GGAATGGGTTGACATGATTGATGCTGGTATTATTGATCCTGTCAAGGTAACTCGTTCAGC 2215

Qy   1514 GCTTCAAAATGCAGCTTCTGTAGCTAGTCTTATTTTGACAACAGAAGCAGTTGTTGCTAA 1573
Db   2216 CCTTCAAAATGCAGCATCTGTAGCTAGTCTCATTTTAACAACAGAAGCCGTTGTGGCGGA 2275

Qy   1574 TAAACCTGAACCAGCTACGCCAGCGCCAGC 1603
Db   2276 TCATCCAGCTCCAGAAGCACCAGCAGCAGC 2305
```

RESULT 15
AF389515
LOCUS AF389515 2320 bp DNA linear BCT 02-JUL-2002
DEFINITION Streptococcus intermedius GroES gene, complete cds; and GroEL gene, partial cds.
ACCESSION AF389515
VERSION AF389515.1 GI:21666291
KEYWORDS .
SOURCE Streptococcus intermedius.
ORGANISM Streptococcus intermedius
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
REFERENCE 1 (bases 1 to 2320)
AUTHORS Teng,L.-J.
TITLE The groESL genes of Streptococcus intermedius
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2320)
AUTHORS Teng,L.-J.
TITLE Direct Submission
JOURNAL Submitted (08-JUN-2001) School of Medical Technology, National Taiwan University College of Medicine, No. 1, Chang-Te Street, Taipei 100, Taiwan
FEATURES Location/Qualifiers
source 1. .2320
/organism="Streptococcus intermedius"
/db_xref="taxon:1338"
CDS 405. .686
/codon_start=1
/transl_table=11
/product="GroES"
/protein_id="AAM73643.1"
/db_xref="GI:21666292"
/translation="MLKPLGDRVVLEVEEKEQKVGGFVIAGAGQDATKTAKVVAVGEG
IRTLNGELVAPSVKAGDTVLVESHVGTEVKDGEEKYLVVNEVNILAIVE"
CDS 719. .>2320
/codon_start=1
/transl_table=11
/product="GroEL"
/protein_id="AAM73644.1"
/db_xref="GI:21666293"
/translation="MAKDIKFSADARSAMVRGVDILADTVKVTLGPKGRNVVLEKSFG
SPLITNDGVTIAKEIELEDHFENMGAKLVSEVASKTNDIAGDGTTTATVLTQAIVREG
IKNVTAGANPIGIRRGIETAVATAVEALKANSVPVSNKEAIAQVAAVSSRSEKVGEYI
SEAMEKVGNDGVITIEESKGMDTELDVVEGMQFDRGYLSQYMVTDNEKMVADLDNPYI
LITDKKISNIQEILPLLENILKTSRPLLIIADDVDGEALPTLVLNKIRGTFNVVAVKA
PGFGDRRKAMLEDIAILTGGTVITEDLGLELKDATIEALGQASKVTVDKDSTVIVEGS
GDAEAIANRVAVIKSQIESVTSEFDKEKLQERLAKLSGGVAVIKVGAATETELKEMKL
RIEDALNATRAAVEEGIVSGGGTAFVNVLDAVAALELEADEATGRNIVLRALEEPVRQ
IALNAGFEGSIVIDRLKNSEVGTGFNAATGEWVNMIEAGIIDPVKVTRSALQNAASVA
SLILTTEAVVASQPEPASPAPAMDPS"
BASE COUNT 731 a 408 c 527 g 654 t
ORIGIN

Query Match 64.3%; Score 1068.6; DB 1; Length 2320;
Best Local Similarity 79.2%; Pred. No. 5.6e-208;

Matches 1269; Conservative 0; Mismatches 334; Indels 0; Gaps 0;

```
Qy     13 ATATGGCAAAAGAAATCAAATTTTCAGCAGATGCGCGTGCTGCCATGGTGCGCGGAGTTG 72
Db    717 AAATGGCAAAAGATATTAAATTTTCAGCAGATGCAAGAAGTGCTATGGTACGTGGTGTCG 776

Qy     73 ATATGTTAGCAGATACCGTCAAAGTAACGCTTGGTCCTAAAGGGCGCAATGTTGTTCTTG 132
Db    777 ATATTTTAGCAGATACCGTTAAAGTAACCTTAGGACCTAAAGGACGCAATGTTGTTCTTG 836

Qy    133 AAAAAGCTTTTGGTTCTCCCTTAATTACTAATGACGGGGTAACCATTGCTAAAGAGATCG 192
Db    837 AGAAATCATTTGGCTCACCCCTCATCACAAATGACGGTGTGACTATTGCCAAAGAAATTG 896

Qy    193 AATTAGAAGATCATTTTGAAAACATGGGAGCAAAATTGGTGTCTGAAGTGGCTTCTAAAA 252
Db    897 AACTCGAAGATCATTTTGAAAATATGGGCGCTAAGTTGGTGTCAGAAGTTGCTTCAAAAA 956

Qy    253 CCAATGATATTGCTGGTGATGGGACGACTACTGCAACAGTTTTGACACAAGCCATTGTTC 312
Db    957 CTAATGATATCGCTGGTGACGGAACAACTACTGCGACTGTCTTGACCCAAGCCATTGTCC 1016

Qy    313 ATGAAGGACTAAAAAATGTGACAGCAGGTGCTAATCCAATTGGTATCCGTCGAGGCATTG 372
Db   1017 GCGAAGGAATCAAAAATGTAACGGCTGGTGCAAACCCAATTGGCATTCGTCGTGGTATTG 1076

Qy    373 AAACAGCAACAGCAACAGCTGTTGAAGCCTTGAAAGCCATTGCTCAACCTGTATCTGGCA 432
Db   1077 AAACAGCTGTTGCAACAGCTGTTGAAGCTTTAAAAGCAAATTCTGTTCCAGTTTCTAATA 1136

Qy    433 AGGAAGCTATTGCTCAGGTCGCTGCAGTATCATCACGCTCTGAAAAAGTTGGAGAGTATA 492
Db   1137 AAGAAGCGATTGCACAAGTTGCTGCTGTCTCATCACGTTCTGAAAAAGTCGGAGAATACA 1196

Qy    493 TCTCAGAAGCTATGGAGCGTGTGGGCAACGATGGTGTGATTACCATCGAAGAATCTCGAG 552
Db   1197 TCTCTGAAGCCATGGAAAAAGTTGGCAACGACGGTGTCATCACTATTGAAGAATCAAAAG 1256

Qy    553 GTATGGAAACAGAACTTGAAGTGGTTGAAGGCATGCAATTTGACCGTGGTTACCTGTCTC 612
Db   1257 GAATGGACACAGAGCTAGATGTTGTTGAAGGTATGCAGTTTGACCGTGGCTATCTTTCTC 1316

Qy    613 AATACATGGTCACAGACAATGAAAAAATGGTTGCAGACCTTGAAAACCCATTTATCTTAA 672
Db   1317 AATACATGGTAACAGACAATGAAAAAATGGTTGCTGATTTAGATAATCCATATATCTTGA 1376

Qy    673 TCACGGATAAAAAAGTGTCAAACATCCAAGACATTTTGCCACTACTTGAGGAAGTTCTTA 732
Db   1377 TTACAGATAAGAAGATTTCTAATATCCAAGAAATTCTTCCTTTGTTGGAAAATATTTTAA 1436

Qy    733 AAACCAACCGTCCATTACTCATTATTGCAGATGATGTGGATGGTGAAGCACTTCCAACCC 792
Db   1437 AAACAAGTCGTCCGCTTTTGATTATTGCAGATGATGTAGATGGTGAAGCTCTTCCAACTC 1496

Qy    793 TTGTCTTGAACAAGATTCGTGGTACTTTCAATGTGGTTGCTGTCAAAGCGCCAGGATTTG 852
Db   1497 TTGTGTTGAACAAAATCCGTGGTACTTTCAATGTAGTCGCTGTGAAAGCGCCAGGATTCG 1556

Qy    853 GTGATCGTCGTAAAGCTATGCTTGAAGACATTGCTATCTTGACAGGTGGTACAGTGATTA 912
Db   1557 GTGACCGTCGTAAGGCGATGCTAGAAGATATTGCGATTTTGACTGGCGGTACAGTGATTA 1616

Qy    913 CAGAGGATCTAGGACTTGAATTAAAAGATGCTACAATGACAGCCCTTGGACAGGCTGCTA 972
Db   1617 CAGAAGATCTTGGTCTGGAATTGAAAGATGCAACCATTGAAGCACTTGGACAAGCCTCAA 1676

Qy    973 AGATTACAGTTGATAAAGATAGCACAGTAATTGTTGAAGGTTCAGGAAGTTCAGAAGCTA 1032
Db   1677 AAGTAACTGTGGATAAAGACAGCACCGTTATCGTTGAAGGCTCTGGTGATGCTGAAGCGA 1736

Qy   1033 TTGCTAACCGTATTGCACTGATTAAATCGCAATTAGAAACAACAACTTCTGACTTTGACC 1092
Db   1737 TTGCTAACCGCGTTGCTGTCATTAAATCGCAAATTGAAAGTGTTACATCTGAATTTGACA 1796
```

```
Qy   1093 GTGAAAAACTACAAGAACGTTTGGCGAAATTAGCTGGTGGTGTAGCTGTTATCAAAGTAG 1152
          ||||||||||||||||||||||||||||||| |.|||||||| ||||| ||||||||||
Db   1797 AAGAAAAACTACAAGAACGTTTGGCGAAATTATCAGGTGGTGTGGCTGTCATCAAAGTAG 1856

Qy   1153 GAGCTCCAACAGAGACAGCTTTAAAAGAAATGAAACTTCGCATTGAGGATGCTCTAAATG 1212
          | ||| ||||||| |||| | ||||||||||||||||||||||| ||||| || ||||
Db   1857 GTGCTGCAACAGAAACAGAACTCAAAGAAATGAAACTTCGCATTGAAGATGCCCTTAATG 1916

Qy   1213 CTACACGTGCAGCCGTTGAAGAAGGTATCGTTGCTGGTGGTGGAACAGCACTTATTACGG 1272
          | || ||||| || |||||||||| || ||  | ||||||||||||||  || | |  |
Db   1917 CAACTCGTGCCGCTGTTGAAGAAGGAATTGTCTCAGGTGGTGGAACAGCCTTTGTGAATG 1976

Qy   1273 TTATTGAAAAAGTAGCAGCTCTTGAGCTTGAGGGCGATGATGCTACTGGACGTAACATTG 1332
          || | ||   ||| || |||||||| || ||||  ||||| || || || || || ||||
Db   1977 TTTTAGATGCAGTTGCCGCTCTTGAACTGGAGGCTGATGAAGCAACAGGTCGCAATATTG 2036

Qy   1333 TGCTTCGTGCTCTAGAAGAGCCTGTACGTCAAATTGCTTTAAATGCTGGGTACGAAGGCT 1392
          |||||||||| | ||||| || || |||||||| ||| | ||||| || |  |||||||
Db   2037 TGCTTCGTGCTTTGGAAGAACCAGTTCGTCAAATCGCTCTCAATGCAGGATTTGAAGGCT 2096

Qy   1393 CCGTAGTTATTGACAAGTTGAAAAACAGCCCTGCAGGAACAGGATTTAATGCTGCAACAG 1452
          |  | || ||||||   |||||||||      | || ||||||||||||||||||||| |
Db   2097 CGATCGTCATTGACCGTTTGAAAAACTCTGAAGTTGGTACAGGATTTAATGCTGCAACTG 2156

Qy   1453 GTGAGTGGGTTGATATGATTAAAACAGGAATCATTGACCCTGTCAAAGTAACACGATCAG 1512
          | || |||||| | |||||| || |||| |||||||||| |||||||| || || || |
Db   2157 GCGAATGGGTTAACATGATTGAAGCAGGGATCATTGACCCAGTCAAAGTCACTCGTTCTG 2216

Qy   1513 CGCTTCAAAATGCAGCTTCTGTAGCTAGTCTTATTTTGACAACAGAAGCAGTTGTTGCTA 1572
          | |||||||||||| || || |||||||| |||||||| ||||||||||||||||||||
Db   2217 CCCTTCAAAATGCTGCGTCAGTAGCTAGCCTTATTTTAACAACAGAAGCAGTTGTTGCTA 2276

Qy   1573 ATAAACCTGAACCAGCTACGCCAGCGCCAGCAATGCCAGCAGG 1615
          ||||| ||||||||||  ||||| || ||||||    || |
Db   2277 GCCAACCAGAACCAGCTAGCCCAGCTCCCGCAATGGATCCAAG 2319
```

Search completed: April 15, 2003, 02:58:36
Job time : 4511.47 secs